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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 WG 7
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Db      28 WG 27

RESULT 115
CNS000ARA
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR21022 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL055937
VERSION
AL055937.1 GI:4936706
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 60)
AUTHORS
Genoscope.
DIRECT SUBMISSION
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoler in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Location/Qualifiers
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 RC 4
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Db      37 RC 36

RESULT 117
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LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04H02 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL099014
VERSION
AL099014.1 GI:5610625
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
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/misc_feature
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Query Match      20.0%; Score 2; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 WG 7
      ||
Db      28 WG 27

RESULT 115
CNS000ARA
LOCUS
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR21022 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL055937
VERSION
AL055937.1 GI:4936706
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Location/Qualifiers
1. .60
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR21022"
/clone_lib="RPCI-98"
/note="end : T7"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 RC 4
      ||
Db      37 RC 36

RESULT 117
CNS0101K
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04H02 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL099014
VERSION
AL099014.1 GI:5610625
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
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AUTHORS
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- Web : www.genoscope.cns.fr)

```

```

COMMENT      Determination of this BAC-end sequence was carried out as part of a
              collaboration with the European Drosophila Genome Project (EDGP) -
              http://www.edgp.ebi.ac.uk --. This Drosophila melanogaster BAC
              library (Dros BAC) was made by Alain Billaud at CEPH (Centre
              d'Etude du Polymorphisme Humain) with funding provided by a MRC
              project grant. The DNA was prepared from embryos by Alain Bucheton
              and Genevieve Payan. It has been constructed in the vector
              pBelOBAC11.

FEATURES     source
              Location/Qualifiers
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ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WG 7
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        15 WG 16

Db

RESULT 118
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LOCUS
DEFINITION      Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04H02 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION      AL099014.1 GI:5610625
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Genoscope.
Direct Submission
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project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.

FEATURES     source
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QY      6 WG 7
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Db

RESULT 120
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LOCUS
DEFINITION      Drosophila melanogaster genome survey sequence T7 end of BAC
BACN05H08 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION      AL099854.1 GI:5611465
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 60)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.

FEATURES     source
              Location/Qualifiers
              1..60
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              /clone="BACN04H02"
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ORIGIN
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Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CW 5
        ||
        4 CW 5

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<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaut at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

#### FEATURES

Location/Qualifiers  
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#### ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5  
 ||  
 Db 59 CW 58

#### RESULT 121

CNS01TCC  
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 DEFINITION  
 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 194D07 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION  
 AL166341.1 GI:7804079

VERSION  
 GSS; genome survey sequence.

KEYWORDS  
 Tetraodon nigroviridis

#### SOURCE

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

#### REFERENCE

1  
 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

20296633

PUBMED

10835645

#### REFERENCE

2  
 Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

20359837

PUBMED

10899143

3 (bases 1 to 60)

#### REFERENCE

Genoscope.

Direct Submission

TITLE

JOURNAL

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))

- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at

<http://www.genoscope.cns.fr/Tetraodon>.

Location/Qualifiers

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/organism="Tetraodon nigroviridis"

/mol\_type="genomic DNA"

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Location/Qualifiers

1. .60

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Location/Qualifiers

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Location/Qualifiers

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/clone="194D07"

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Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                Saurin,W., Bernot,A., Wincker,P., Brottier,P., Quetier,F.,
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TITLE         Estimate of human gene number provided by genome-wide analysis
                using Tetraodon nigroviridis DNA sequence
JOURNAL       Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE       20296633
PUBMED        10835645
REFERENCE
2
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                Saurin,W., Bernot,A. and Weissenbach,J.
TITLE         Characterization and repeat analysis of the compact genome of the
                freshwater pufferfish Tetraodon nigroviridis
JOURNAL       Genome Res. 10 (7), 939-949 (2000)
MEDLINE       20359837
PUBMED        10899143
REFERENCE
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Direct Submission
JOURNAL       Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
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                http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1. .60
/organism="Tetraodon nigroviridis"
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CW 5
Db 13 CW 12
RESULT 126
CNS02K40/C
LOCUS      Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
DEFINITION 144B24 of library G from Tetraodon nigroviridis, genomic survey
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ACCESSION  AL201033
VERSION     AL201033.1 GI:7859378
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
ORGANISM    Tetraodon nigroviridis
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                Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
                Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                Saurin,W. and Weissenbach,J.
TITLE         Estimate of human gene number provided by genome-wide analysis
                using Tetraodon nigroviridis DNA sequence
JOURNAL       Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE       20296633
PUBMED        10835645
REFERENCE
2
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                Saurin,W., Bernot,A. and Weissenbach,J.
TITLE         Characterization and repeat analysis of the compact genome of the
                freshwater pufferfish Tetraodon nigroviridis
JOURNAL       Genome Res. 10 (7), 939-949 (2000)
MEDLINE       20359837
PUBMED        10899143
REFERENCE
3 (bases 1 to 60)
Genoscope.
Direct Submission
JOURNAL       Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT       This sequence is a single read and was generated as part of a large
                scale clone-end sequencing project of the Tetraodon nigroviridis
                genome. For more information, please take a look at
                http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1. .60
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="144B24"
/clone_lib="G"
/note="Genoscope sequence ID : COAG144DA12SP1-end :
PUC-Ori"
ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 WG 7
Db 12 WG 13
RESULT 126
CNS02K40/C
LOCUS      Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
DEFINITION 144B24 of library G from Tetraodon nigroviridis, genomic survey
                sequence.
ACCESSION  AL201033
VERSION     AL201033.1 GI:7859378
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
ORGANISM    Tetraodon nigroviridis
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
                Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                Saurin,W. and Weissenbach,J.
TITLE         Estimate of human gene number provided by genome-wide analysis
                using Tetraodon nigroviridis DNA sequence
JOURNAL       Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE       20296633
PUBMED        10835645
Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                Saurin,W., Bernot,A. and Weissenbach,J.
TITLE         Characterization and repeat analysis of the compact genome of the
                freshwater pufferfish Tetraodon nigroviridis
JOURNAL       Genome Res. 10 (7), 939-949 (2000)
MEDLINE       20359837
PUBMED        10899143
REFERENCE
3 (bases 1 to 60)
Genoscope.
Direct Submission
JOURNAL       Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT       This sequence is a single read and was generated as part of a large
                scale clone-end sequencing project of the Tetraodon nigroviridis
                genome. For more information, please take a look at
                http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1. .60
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="144B24"
/clone_lib="G"
/note="Genoscope sequence ID : COAG144DA12SP1-end :
PUC-Ori"
ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CW 5
Db 13 CW 12
RESULT 127
CNS02O1W
LOCUS      Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
DEFINITION 153N19 of library G from Tetraodon nigroviridis, genomic survey
                sequence.
ACCESSION  AL206753
VERSION     AL206753.1 GI:7865572
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
ORGANISM    Tetraodon nigroviridis
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
                Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                Saurin,W. and Weissenbach,J.
TITLE         Estimate of human gene number provided by genome-wide analysis
                using Tetraodon nigroviridis DNA sequence
JOURNAL       Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE       20296633
PUBMED        10835645
REFERENCE
2
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                Saurin,W., Bernot,A. and Weissenbach,J.
TITLE         Characterization and repeat analysis of the compact genome of the
                freshwater pufferfish Tetraodon nigroviridis
JOURNAL       Genome Res. 10 (7), 939-949 (2000)
MEDLINE       20359837
PUBMED        10899143
REFERENCE
3 (bases 1 to 60)

```

AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequençage : Bp.191 91006 EVRY cedex - FRANCE (E-mail : <a href="mailto:segref@genoscope.cns.fr">segref@genoscope.cns.fr</a> )
COMMENT	Web : <a href="http://www.genoscope.cns.fr">www.genoscope.cns.fr</a> This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetradon">http://www.genoscope.cns.fr/Tetradon</a> .
REMARKS	

```

... source
location/Qualifiers
1..60
organism="Tetraodon nigroviridis"
mol_type="genomic DNA"
db_xref="taxon:99883"
clone_lib="ng"
notes="Genoscope sequence ID : COAG153G10SF1-end :
pUC-ori="

```

Query Match	20.0%	Score 2	DB 9	Length 60
Best Local Similarity	100.0%	Pred.No. 0		
Matches	2	Conservative 0	Mismatches 0	Indels 0
				Gaps 0

QY 4 CW 5  
DB 58 CW 59

RESULT 128  
CNS020IW/c  
LOCUS  
DEFINITION  
CNS020IW 60 bp DNA linear GSS 01-SEP-2000  
Tetraodon nigroviridis genome survey sequence PUC-Orl end of clone  
13N19 of library G from Tetraodon nigroviridis, genomic survey  
sequence.

ACCESSION  
AL206753  
VERSION  
AL206753.1  
KEYWORDS  
GSS: genome survey sequence.  
SOURCE  
Tetraodon nigroviridis  
ORGANISM  
Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

MEDLINE	20296633	Roest Crollius, H., Jallou, O., Dasilva, C., Ozouf-Costaz, C.,
PUBMED	10835645	Fizames, C., Fischer, C., Bouneau, L., Billault, A., Querier, F.,
REFERENCE	2	Saurin, W., Bernot, A. and Weissenbach, J.
AUTHORS		Characterization and repeat analysis of the compact genome of the
		freshwater pufferfish Tetraodon nigroviridis
TITLE		Genome Res. 10 (7), 939-949 (2000)
JOURNAL		

20359837  
MEDLINE  
PUBMED  
10899143  
3 (bases 1 to 60)  
REFERENCE  
Genoscope,  
AUTHORS  
TITLE  
Direct Submission  
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
BP 131 91006 EVRY cedex - FRANCE (E-mail : [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr)  
Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
COMMENT  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/tetraodon>.  
FEATURES  
Location/Qualifiers

```

source
1. 50
/organism="Tetraodon nigroviridis"
/ncbi_taxid="9606"
/db_xref="taxon:99883"
/clone_lib="N19"
/clone="153N19"
/note="Genoscope sequence ID : COAG153CG10SP1-end :
pUC-ori"

```

```

Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 WG 7
          ||
          59 WG 58

Db

```

RESULT 129  
CN50330M  
LOCUS  
DEFINITION  
CN50330M 60 bp DNA linear GSS 01-SEP-2000  
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
208105 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
ACCESSION  
AL225535  
VERSION  
AL225535.1 GI:7884433  
KEYWORDS  
GSS; genome survey sequence.

SOURCE ORGANISM

Tetraodon nigroviridis  
Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontoideae; Tetraodontidae; Tetraodon

REFERENCE  
AUTHORS  
Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,  
Bernot, A., Fraznes, C., Winckel, P., Brottier, P., Quetier, F.,  
Saurin, W. and Weissenbach, J.  
TITLE  
Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence  
JOURNAL  
Nat. Genet. 25 (2), 235-238 (2000)

MEDLINE	20296633	Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C.,
PUBLISHED	10835645	Fizames, C., Fischer, C., Bouneau, R., Billault, A., Quetier, F.,
REFERENCE	2	Saurin, W., Barnot, A. and Weissenbach, J.
AUTHORS		Characterization and repeat analysis of the compact genome of the
		freshwater puifish Tetraodon lineatus
TITLE		Genome Res. 10 (7), 939-949 (2000)
JOURNAL		

MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	20359837 10899143 3 (bases 1 to 60) Genoscope. Direct Submission Submitted (12-APR-2000) BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr) - Web : www.genoscope.cns.fr)	Genoscope - Centre National de Sequencage : This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetraodon">http://www.genoscope.cns.fr/Tetraodon</a> .
COMMENT		

```

FEATURES
    source
    Location/Qualifiers
        1..60
            /organism="Tetraodon nigroviridis"
            /mol_type="Genomic DNA"
            /db_xref="taxon:99883"
            /clone="208105"
            /clone_lib="G"
            /note="Genoscope sequence ID : COAG208AE03SP1-end :
            pUC-ori"

```



Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodontidae; Tetraodon.

# REFERENCE AUTHORS

## TITLE

Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence

# JOURNAL MEDLINE PUBMED

Nat. Genet. 25 (2), 235-238 (2000)

# REFERENCE AUTHORS

Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fischer, C.,  
Barnot, A., Fzames, C., Wincker, P., Brottier, P., Quetier, F.,  
Saurin, W., Bernot, A. and Weissenbach, J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis

# JOURNAL MEDLINE PUBMED

Genome Res. 10 (7), 939-949 (2000)

# REFERENCE AUTHORS

Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fischer, C.,  
Fzames, C., Fischer, C., Wincker, P., Brottier, P., Quetier, F.,  
Saurin, W., Bernot, A. and Weissenbach, J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis

# JOURNAL MEDLINE PUBMED

Genome Res. 10 (7), 939-949 (2000)

# REFERENCE AUTHORS

Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence

# JOURNAL MEDLINE PUBMED

Nat. Genet. 25 (2), 235-238 (2000)

## ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# Qy 7 GY 8 Db 11 GY 10

## RESULT 133 CNS03QDZ

# LOCUS

Tetraodon nigroviridis genome survey sequence PUC-ORI end of clone  
047M23 of library G from Tetraodon nigroviridis, genomic survey  
sequence.

# ACCESSION VERSION

# KEYWORDS

# SOURCE

# ORGANISM

# REFERENCE AUTHORS

Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fischer, C.,  
Barnot, A., Fzames, C., Wincker, P., Brottier, P., Quetier, F.,  
Saurin, W., Bernot, A. and Weissenbach, J.  
Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence

# JOURNAL MEDLINE PUBMED

Nat. Genet. 25 (2), 235-238 (2000)

## REFERENCE AUTHORS

## TITLE

Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence

## JOURNAL MEDLINE PUBMED

## REFERENCE AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Qy 7 GY 8 Db 11 GY 12

## RESULT 134 CNS03QDZ/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Qy 7 GY 8 Db 11 GY 12

## RESULT 134 CNS03QDZ/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Qy 7 GY 8 Db 11 GY 12

## RESULT 134 CNS03QDZ/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Qy 7 GY 8 Db 11 GY 12

## RESULT 134 CNS03QDZ/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Qy 7 GY 8 Db 11 GY 12

## RESULT 134 CNS03QDZ/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Qy 7 GY 8 Db 11 GY 12

## RESULT 134 CNS03QDZ/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Qy 7 GY 8 Db 11 GY 12

## RESULT 134 CNS03QDZ/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Qy 7 GY 8 Db 11 GY 12

## RESULT 134 CNS03QDZ/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Qy 7 GY 8 Db 11 GY 12

## RESULT 134 CNS03QDZ/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## REFERENCE AUTHORS

## TITLE

## JOURNAL MEDLINE PUBMED

## COMMENT

## FEATURES

## source

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Qy 7 GY 8 Db 11 GY 12

## RESULT 134 CNS03QDZ/c

## LOCUS

## DEFINITION

## ACCESSION

```

REFERENCE 3 (bases 1 to 60)
AUTHORS   Genoscope.
TITLE     Direct Submission
JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT   This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES   Location/Qualifiers
            source
            1..60
            /organism="Tetraodon nigroviridis"
            /mol_type="genomic DNA"
            /db_xref="taxon:99883"
            /clone="047M23"
            /clone_lib="G"
            /note="Genoscope sequence ID : COBG047AG12SPI-end :
PUC-ori"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RC 4
      ||
      12 RC 11

RESULT 135
AY431565
LOCUS       AY431565               61 bp mRNA linear      HTC 24-JUN-2004
DEFINITION   Aedes aegypti ASAP ID: 38007 unknown mRNA sequence.
ACCESSION   AY431565
VERSION     AY431565.1 GI:42763707
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1 (bases 1 to 61)
AUTHORS     Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-P., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
TITLE       Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
JOURNAL     Infect. Immun. 72 (7), 4114-4126 (2004)
PUBMED     15213157
REFERENCE   2 (bases 1 to 61)
AUTHORS     Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-P., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
TITLE       Direct Submission
JOURNAL     Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.

FEATURES   Location/Qualifiers
            source
            1..61
            /organism="Aedes aegypti"
            /mol_type="mRNA"
            /strain="liverpool"
            /isolation_source="perfused hemolymph of
            bacteria-inoculated organisms at 1, 3, 6, 12, and 24
            hours post-inoculation"
            /db_xref="taxon:7159"
            /sex="female"
            /cell_type="hemocyte"
            /tissue_type="hemolymph"
            /dev_stage="adult"
            /note="ASAP-UW Feature ID: 38006"

misc_feature
            1..61
            /note="unknown; ASAP-UW Feature ID: 38007"

ORIGIN
Query Match      20.0%; Score 2; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GV 8
      ||
      26 GV 27

RESULT 136
AY431565/c
LOCUS       AY431565/c           61 bp mRNA linear      HTC 24-JUN-2004
DEFINITION   Aedes aegypti ASAP ID: 38007 unknown mRNA sequence.
ACCESSION   AY431565
VERSION     AY431565.1 GI:42763707
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1 (bases 1 to 61)
AUTHORS     Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
TITLE       Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
JOURNAL     Infect. Immun. 72 (7), 4114-4126 (2004)
PUBMED     15213157
REFERENCE   2 (bases 1 to 61)
AUTHORS     Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
TITLE       Direct Submission
JOURNAL     Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.

FEATURES   Location/Qualifiers
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            hours post-inoculation"
            /db_xref="taxon:7159"
            /sex="female"
            /cell_type="hemocyte"
            /tissue_type="hemolymph"
            /dev_stage="adult"
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ORIGIN

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 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RC 4  
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 27 RC 26

Db

RESULT 137  
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 LOCUS  
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 ACCESSION AY432562  
 VERSION AY432562.1 GI:42763799  
 KEYWORDS  
 SOURCE  
 ORGANISM Aedes aegypti (yellow fever mosquito)  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;  
 Stegomyia.  
 1 (bases 1 to 61)  
 Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,  
 Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,  
 Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,  
 Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and  
 Christensen,B.M.  
 Description of the Transcriptomes of Immune Response-Activated  
 Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres  
 subalbatus  
 Infect. Immun. 72 (7), 4114-4126 (2004)  
 15213157  
 2 (bases 1 to 61)  
 Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,  
 Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,  
 Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,  
 Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and  
 Christensen,B.M.  
 Direct Submission  
 Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,  
 University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI  
 53706, USA  
 More information about this sequence is available in ASAP (A  
 Systematic Annotation Package for community analysis of genomes)  
 from the University of Wisconsin-Madison at  
 https://asap.shabs.wisc.edu/annotation/php/logon.php.

FEATURES  
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 /cell\_type="hemocyte"  
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ORIGIN  
 Query Match 20.0%; Score 2; DB 3; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 0;  
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QY 3 RC 4  
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 27 RC 28

Db

RESULT 138  
 AY432562/c  
 LOCUS  
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 ACCESSION AY432562  
 VERSION AY432562.1 GI:42763799  
 KEYWORDS  
 SOURCE  
 ORGANISM Aedes aegypti (yellow fever mosquito)  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;  
 Stegomyia.  
 1 (bases 1 to 61)  
 Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,  
 Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,  
 Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,  
 Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and  
 Christensen,B.M.  
 Description of the Transcriptomes of Immune Response-Activated  
 Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres  
 subalbatus  
 Infect. Immun. 72 (7), 4114-4126 (2004)  
 15213157  
 2 (bases 1 to 61)  
 Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,  
 Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,  
 Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,  
 Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and  
 Christensen,B.M.  
 Direct Submission  
 Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,  
 University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI  
 53706, USA  
 More information about this sequence is available in ASAP (A  
 Systematic Annotation Package for community analysis of genomes)  
 from the University of Wisconsin-Madison at  
 https://asap.shabs.wisc.edu/annotation/php/logon.php.

FEATURES  
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 /db\_xref="taxon:7159"  
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 /tissue\_type="hemolymph"  
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ORIGIN  
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 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 8  
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 28 GY 27

Db

RESULT 139  
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 LOCUS  
 DEFINITION Aedes aegypti 61 bp mRNA linear HTC 24-JUN-2004  
 ACCESSION AY432871  
 VERSION AY432871.1 GI:42763173  
 KEYWORDS  
 SOURCE  
 ORGANISM Aedes aegypti (yellow fever mosquito)  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.

REFERENCE 1 (bases 1 to 61)  
 AUTHORS Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.

TITLE Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors *Aedes aegypti* and *Armigeres subalbatus*

JOURNAL Infect. Immun. 72 (7), 4114-4126 (2004)  
 PUBMED 15213157  
 REFERENCE 2 (bases 1 to 61)  
 AUTHORS Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Rusch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Kuo, H.-K., Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.

TITLE Direct Submission

JOURNAL Submitted (08-OCT-2003) Animal Health and Biomedical Sciences, University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI 53706, USA

COMMENT More information about this sequence is available in ASAP (A Systematic Annotation Package for community analysis of genomes) from the University of Wisconsin-Madison at <https://asap.ababs.wisc.edu/annotation/php/logon.php>.

FEATURES  
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ORIGIN

Query Match 20.0%; Score 2; DB 3; Length 61;  
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 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 8  
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 Db 17 GY 18

RESULT 140  
 AY432871/c  
 LOCUS AY432871 61 bp mRNA linear HTC 24-JUN-2004  
 DEFINITION *Aedes aegypti* ASAP ID: 35499 unknown mRNA sequence.  
 ACCESSION AY432871  
 VERSION AY432871.1 GI:42763173  
 KEYWORDS HTC.  
 SOURCE *Aedes aegypti* (yellow fever mosquito)  
 ORGANISM *Aedes aegypti*  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.

REFERENCE 1 (bases 1 to 61)  
 AUTHORS Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.

TITLE Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors *Aedes aegypti* and *Armigeres*

subalbatus

JOURNAL Infect. Immun. 72 (7), 4114-4126 (2004)  
 PUBMED 15213157  
 REFERENCE 2 (bases 1 to 61)  
 AUTHORS Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Rusch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Kuo, H.-K., Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.

TITLE Direct Submission

JOURNAL Submitted (08-OCT-2003) Animal Health and Biomedical Sciences, University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI 53706, USA

COMMENT More information about this sequence is available in ASAP (A Systematic Annotation Package for community analysis of genomes) from the University of Wisconsin-Madison at <https://asap.ababs.wisc.edu/annotation/php/logon.php>.

FEATURES  
 source  
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 /db\_xref="taxon:7159"  
 /sex="female"  
 /cell\_type="hemocyte"  
 /tissue\_type="hemolymph"  
 /dev\_stage="adult"  
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misc\_feature 1..61  
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ORIGIN

Query Match 20.0%; Score 2; DB 3; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4  
 ||  
 Db 18 RC 17

RESULT 141  
 L76124  
 LOCUS L76124 61 bp mRNA linear EST 21-FEB-1996  
 DEFINITION SCMRAP0218 G2/KS adult worm mini-library Schistosoma mansoni cDNA clone SMRAP0218, mRNA sequence.  
 ACCESSION L76124  
 VERSION L76124.1 GI:1196862  
 KEYWORDS EST.  
 SOURCE Schistosoma mansoni  
 ORGANISM Schistosoma mansoni  
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida; Schistosomatoidea; Schistosomatidae; Schistosoma.

REFERENCE 1 (bases 1 to 61)  
 AUTHORS Neto, E.D., Harrop, R., Correa-Oliveira, R., Wilson, R.A., and Simpson, A.J.G.

TITLE Minilibraries constructed from cDNA generated by arbitrarily primed RT-PCR: an alternative to normalized libraries for the generation of ESTs from nanogram quantities of mRNA

JOURNAL Gene 186 (1), 135-142 (1997)  
 MEDLINE 97199380  
 PUBMED 9047356  
 COMMENT Contact: Neto, E.D., Harrop, R., Correa-Oliveira, R., Wilson, R.A., Pena, S.D. and Simpson, A.J.G.

FEATURES  
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/note="A mini-library was made by cloning products derived from RNA-arbitrarily primed PCR (RAP PCR) profiles into the pUC 18 vector. Reverse transcription of adult worm mRNA was primed with G2and subsequent PCR amplification was performed in the presence of primer KS"

## ORIGIN

Query Match 20.0%; Score 2; DB 7; Length 61;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 GY 8  
Db 34 GY 35

RESULT 142  
L76124/c

LOCUS L76124 61 bp mRNA linear EST 21-FEB-1996  
DEFINITION SCMRAP0218 G2/KS adult worm mini-library Schistosoma mansoni CDNA  
clone SMRAP0218, mRNA sequence.

ACCESSION L76124  
VERSION L76124.1 GI:1196862

KEYWORDS EST.

SOURCE Schistosoma mansoni

ORGANISM Schistosoma mansoni

REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

AUTHORS Strigoidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

TITLE Neto,E.D., Harrop,R., Correa-Oliveira,R, Wilson,R.A., Pena,S.D. and Simpson,A.J.G.

JOURNAL Mini-libraries constructed from cDNA generated by arbitrarily primed RT-PCR: an alternative to normalized libraries for the generation of ESTs from nanogram quantities of mRNA

MEDLINE Gene 186 (1), 135-142 (1997)

PUBMED 97199380

COMMENT 9047356

Contact: Neto,E.D., Harrop,R., Correa-Oliveira,R., Wilson,R.A., Pena,S.D. and Simpson,A.J.

FEATURES  
source

1. .61  
Location/Qualifiers  
/organism="Schistosoma mansoni"  
/mol\_type="mRNA"  
/db\_xref="taxon:6183"  
/clone="SMRAP0218"  
/clone\_lib="G2/KS adult worm mini-library"  
/note="A mini-library was made by cloning products derived from RNA-arbitrarily primed PCR (RAP PCR) profiles into the pUC 18 vector. Reverse transcription of adult worm mRNA was primed with G2and subsequent PCR amplification was performed in the presence of primer KS"

## ORIGIN

Query Match 20.0%; Score 2; DB 7; Length 61;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 RC 4  
Db 44 RC 43

## RESULT 143

## CNS0139J

## LOCUS

DEFINITION CNS0139J 61 bp DNA linear GSS 26-JUL-1999  
Drosophila melanogaster genome survey sequence T7 end of BAC  
BACN09E06 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION AL102577

VERSION AL102577.1 GI:5614188

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

REFERENCE  
AUTHORSTITLE  
JOURNAL

## COMMENT

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1. (bases 1 to 61)  
Genoscope.

Direct Submission  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBelobAC11.

## FEATURES

## source

1. .61  
Location/Qualifiers  
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## ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 61;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 WG 7  
Db 47 WG 48

## RESULT 144

## CNS0139J/c

## LOCUS

## DEFINITION

CNS0139J 61 bp DNA linear GSS 26-JUL-1999  
Drosophila melanogaster genome survey sequence T7 end of BAC  
BACN09E06 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION AL102577.1 GI:5614188

VERSION GSS.

KEYWORDS Drosophila melanogaster (fruit fly)

SOURCE Drosophila melanogaster

ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1. (bases 1 to 61)  
Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the European Drosophila Genome Project (EDGP) -

http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC

library (Dros BAC) was made by Alain Billaud at CEPH (Centre

d'Etude du Polymorphisme Humain) with funding provided by a MRC

project grant. The DNA was prepared from embryos by Alain Bucheton

and Genevieve Payan. It has been constructed in the vector

pBelobAC11.

Location/Qualifiers

1. .61

/organism="Drosophila melanogaster"

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ORIGIN
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5
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Db 48 CW 47

RESULT 145
CNS02J97
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
143G23 of library G from Tetraodon nigroviridis, genomic survey
sequence.

Qy 4 CW 5
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Db 48 CW 47

RESULT 146
CNS02J97/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
143G23 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION
AL199924
VERSION
AL199924.1 GI:7838075
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.

REFERENCE
1
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
PUBMED
10835645
2
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
20359837
PUBMED
10899143
3 (bases 1 to 61)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source
1..61
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/db_xref="taxon:99883"
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/clone_lib="G"
/note="Genoscope sequence ID : COAG143AD12SP1-end :
PUC-Ori"

ORIGIN
Query Match          20.0%; Score 2; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5
    ||
Db 23 CW 22

RESULT 147
CNS02MP4
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
149J04 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION
AL204385
VERSION
AL204385.1 GI:7863204

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KEYWORDS
SOURCE      GSS; genome survey sequence.
ORGANISM    Tetraodon nigroviridis

REFERENCE
AUTHORS     Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
            Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
            Nat. Genet. 25 (2), 235-238 (2000)
            20296633
            PUBMED
            10835645
            REFERENCE
            2

TITLE
JOURNAL     Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
MEDLINE     Fizames,C., Fischer,C., Wincker,P., Brottier,P., Quetier,F.,
PUBMED      Saurin,W. and Weissenbach,J.
            Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
            Nat. Genet. 25 (2), 235-238 (2000)
            20296633
            PUBMED
            10835645
            REFERENCE
            2

AUTHORS     Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
            Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
            Genome Res. 10 (7), 939-949 (2000)
            20359837
            PUBMED
            10899143
            REFERENCE
            3 (bases 1 to 61)
            Genoscope.
            Direct Submission
            Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
            This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source
1. .61
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   /mol_type="genomic DNA"
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   /clone="149J04"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WG 7
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Db      22 WG 21

RESULT 149
CNS03955
LOCUS
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            006P23 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
            AL233474.1 GI:7892609
            GSS: genome survey sequence.
            Tetraodon nigroviridis
            Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodontidae; Tetraodon.
            1
            REFERENCE
            1
            AUTHORS
            Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
            Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
            Nat. Genet. 25 (2), 235-238 (2000)
            20296633
            PUBMED
            10835645
            REFERENCE
            2

AUTHORS     Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
            Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
            Genome Res. 10 (7), 939-949 (2000)
            20359837
            PUBMED
            10899143
            REFERENCE
            3 (bases 1 to 61)
            Genoscope.
            Direct Submission
            Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
            This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source
1. .61
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   /db_xref="taxon:99883"
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   /clone_lib="G"
   /notes="Genoscope sequence ID : COAG149DE02LP1-end : T7"

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CW 5
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Db      21 CW 22

RESULT 148
CNS02MP4/c
LOCUS
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
            149J04 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
            AL204385.1 GI:7863204
            GSS: genome survey sequence.
            Tetraodon nigroviridis
            Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodontidae; Tetraodon.
            1
            REFERENCE
            1
            AUTHORS
            Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.

```

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JOURNAL      Genome Res. 10 (7), 939-949 (2000)
MEDLINE      20359837
PUBMED       10899143
REFERENCE    3 (bases 1 to 61)
AUTHORS      Genoscope.
TITLE        Direct Submission
JOURNAL      Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
              BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
              - Web : www.genoscope.cns.fr)
COMMENT      This sequence is a single read and was generated as part of a large
              scale clone-end sequencing project of the Tetraodon nigroviridis
              genome. For more information, please take a look at
              http://www.genoscope.cns.fr/Tetraodon.
FEATURES     source
              1. .61
              /organism="Tetraodon nigroviridis"
              /mol_type="genomic DNA"
              /db_xref="taxon:99883"
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              /clone_lib="G"
              /note="Genoscope sequence ID : COBG006CH12SP1-end :
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Query Match      20.0%; Score 2; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY              3 RC 4
              ||
Db              56 RC 57
RESULT 150
CNS03955/c
LOCUS          CNS03955      61 bp      DNA      linear      GSS 01-SEP-2000
DEFINITION    Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
              006P23 of library G from Tetraodon nigroviridis, genomic survey
              sequence.
ACCESSION     AL233474.1 GI:7892609
VERSION       AL233474.1
KEYWORDS      GSS; genome survey sequence.
SOURCE        Tetraodon nigroviridis
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
              Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE     1
AUTHORS       Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
              Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
              Saurin,W. and Weissenbach,J.
TITLE         Estimate of human gene number provided by genome-wide analysis
              using Tetraodon nigroviridis DNA sequence
JOURNAL       Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE       20296633
PUBMED        10835645
REFERENCE     2
AUTHORS       Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
              Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
              Saurin,W., Bernot,A. and Weissenbach,J.
TITLE         Characterization and repeat analysis of the compact genome of the
              freshwater pufferfish Tetraodon nigroviridis
JOURNAL       Genome Res. 10 (7), 939-949 (2000)
MEDLINE       20359837
PUBMED        10899143
REFERENCE     3 (bases 1 to 61)
AUTHORS      Genoscope.
TITLE        Direct Submission
JOURNAL      Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
              BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
              - Web : www.genoscope.cns.fr)
COMMENT      This sequence is a single read and was generated as part of a large
              scale clone-end sequencing project of the Tetraodon nigroviridis
              genome. For more information, please take a look at
              http://www.genoscope.cns.fr/Tetraodon.
FEATURES     source
              1. .61
              /organism="Tetraodon nigroviridis"
              /mol_type="genomic DNA"
              /db_xref="taxon:99883"
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              /clone_lib="G"
              /note="Genoscope sequence ID : COBG006CH12SP1-end :
              PUC-Ori"
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Query Match      20.0%; Score 2; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY              3 RC 4
              ||
Db              56 RC 57
RESULT 151
CNS03UDP
LOCUS          CNS03UDP      61 bp      DNA      linear      GSS 01-SEP-2000
DEFINITION    Tetraodon nigroviridis genome survey sequence T7 end of clone
              058P02 of library G from Tetraodon nigroviridis, genomic survey
              sequence.
ACCESSION     AL260998
VERSION       AL260998.1 GI:7982623
KEYWORDS      GSS; genome survey sequence.
SOURCE        Tetraodon nigroviridis
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
              Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE     1
AUTHORS       Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
              Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
              Saurin,W. and Weissenbach,J.
TITLE         Estimate of human gene number provided by genome-wide analysis
              using Tetraodon nigroviridis DNA sequence
JOURNAL       Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE       20296633
PUBMED        10835645
REFERENCE     2
AUTHORS       Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
              Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
              Saurin,W., Bernot,A. and Weissenbach,J.
TITLE         Characterization and repeat analysis of the compact genome of the
              freshwater pufferfish Tetraodon nigroviridis
JOURNAL       Genome Res. 10 (7), 939-949 (2000)
MEDLINE       20359837
PUBMED        10899143
REFERENCE     3 (bases 1 to 61)
AUTHORS      Genoscope.
TITLE        Direct Submission
JOURNAL      Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
              BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
              - Web : www.genoscope.cns.fr)
COMMENT      This sequence is a single read and was generated as part of a large
              scale clone-end sequencing project of the Tetraodon nigroviridis
              genome. For more information, please take a look at
              http://www.genoscope.cns.fr/Tetraodon.
FEATURES     source
              1. .61
              /organism="Tetraodon nigroviridis"
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/note="Genoscope sequence ID : COBG058DC01LP1-end : T7"

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RC 4
   ||
Db 3 RC 4

RESULT 152
CNS030UDP/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
058F02 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL260398
VERSION
AL260398.1 GI:7982623
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
1
REFERENCE
1 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bertot,A., Fzames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
PUBMED
10835645
REFERENCE
2
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bertot,A., Fzames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
PUBMED
10835645
REFERENCE
3 (bases 1 to 61)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
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Query Match      20.0%; Score 2; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CY 8
   ||
Db 4 CY 3

RESULT 154
CNS044FV/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
081B01 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL274036
VERSION
AL274036.1 GI:7996303
KEYWORDS
GSS; genome survey sequence.

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**SOURCE**  
ORGANISM Tetraodon nigroviridis

**REFERENCE**  
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fzames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.  
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)  
MEDLINE 20296633  
PUBMED 10835645

**REFERENCE**  
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Fzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Genome Res. 10 (7), 939-949 (2000)  
MEDLINE 20359837  
PUBMED 10899143

**REFERENCE**  
3 (bases 1 to 61)  
GENOSCOPE  
Direct Submission  
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

**FEATURES**  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 RC 4  
||  
Db 37 RC 36

**RESULT 155**  
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LOCUS AW059587 62 bp mRNA linear EST 23-AUG-2000  
DEFINITION HuTH.bsst.dnc15.final.cluster.77 (3) DNC15 Homo sapiens cDNA similar to ribosomal protein L23A, mRNA sequence.  
ACCESSION AW059587  
VERSION AW059587.1 GI:6651909  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 62)  
Brenner,S., Williams,S.R., Vermaas,E.H., Storck,T., Moon,K., McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B., Burcham,T. and Albrecht,G.  
In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs  
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

**REFERENCE**  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 62)  
Brenner,S., Williams,S.R., Vermaas,E.H., Storck,T., Moon,K., McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B., Burcham,T. and Albrecht,G.  
In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs  
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

**MEDLINE**  
PUBMED 20144098  
COMMENT Contact: Burcham TS  
LYNX Therapeutics, Inc.  
25861 Industrial Blvd., Hayward, CA 94545, USA  
Tel: 510 670 9338  
Fax: 510 670 9302  
Email: timb@lynxgen.com  
Sequence obtained from LYNX Therapeutics Megasort technology. Collected from the down-regulated gate. Consensus sequence of 3 sequences in cluster.  
High quality sequence stop: 62.  
Location/Qualifiers  
1. .62  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="monocytic leukemia"  
/cell\_line="THP-1 (TIB-202)"  
/clone\_lib="DNC15"  
/note="Vector: pCR2.1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."

**ORIGIN**  
Query Match 20.0%; Score 2; DB 2; Length 62;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 RC 4  
||  
Db 21 RC 22

**RESULT 156**  
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LOCUS AW059587 62 bp mRNA linear EST 23-AUG-2000  
DEFINITION HuTH.bsst.dnc15.final.cluster.77 (3) DNC15 Homo sapiens cDNA similar to ribosomal protein L23A, mRNA sequence.  
ACCESSION AW059587  
VERSION AW059587.1 GI:6651909  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 62)  
Brenner,S., Williams,S.R., Vermaas,E.H., Storck,T., Moon,K., McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B., Burcham,T. and Albrecht,G.  
In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs  
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

**REFERENCE**  
AUTHORS LYNX Therapeutics, Inc.  
25861 Industrial Blvd., Hayward, CA 94545, USA  
Tel: 510 670 9338  
Fax: 510 670 9302  
Email: timb@lynxgen.com  
Sequence obtained from LYNX Therapeutics Megasort technology. Collected from the down-regulated gate. Consensus sequence of 3 sequences in cluster.  
High quality sequence stop: 62.  
Location/Qualifiers  
1. .62  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="monocytic leukemia"  
/cell\_line="THP-1 (TIB-202)"  
/clone\_lib="DNC15"

**FEATURES**  
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1. .62  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="monocytic leukemia"  
/cell\_line="THP-1 (TIB-202)"  
/clone\_lib="DNC15"

/note="Vector: PCR2.1; Cloning of PCR products from micro-beads carrying 3', end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."

## ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 62;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 WG 7  
Db 61 WG 60

## RESULT 157

AW059628 HUTH.bsst.dnc15.final.cluster\_118\_2) DNC15 Homo sapiens cDNA, mRNA  
LOCUS  
DEFINITION

sequence.

## ACCESSION

AW059628

## VERSION

EST.

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Brenner, S., Williams, S.R., Vermaas, E.H., Storck, T., Moon, K.,

McCollum, C., Mao, J.I., Kirchner, J.J., Elettr, S., DuBridge, R.B.,

Burcham, T. and Albrecht, G.

In vitro cloning of complex mixtures of DNA on microbeads: Physical

separation of differentially expressed cDNAs

Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

20144098

10677516

Contact: Burcham TS

LYNX Therapeutics, Inc.

25861 Industrial Blvd., Hayward, CA 94545, USA

Tel: 510 670 9338

Fax: 510 670 9302

Email: timb@lynxgen.com

Sequence obtained from LYNX Therapeutics Megasort technology.

Collected from the down-regulated gate. Consensus sequence of 2

sequences in cluster.

High quality sequence stop: 62.

Location/Qualifiers

1..62

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/cell\_type="monocytic leukemia"

/cell\_line="THP-1 (TIB-202)"

/clone\_lib="DNC15"

/note="Vector: PCR2.1; Cloning of PCR products from

micro-beads carrying 3', end of down-regulated cDNA. THP-1

cells non-induced (treated with DMSO only)."

QY 7 GY 8

Db 61 GY 62

## RESULT 158

AW059628/c  
LOCUS  
DEFINITION

sequence.

AW059628

HUTH.bsst.dnc15.final.cluster\_118\_2) DNC15 Homo sapiens cDNA, mRNA

sequence.

AW059628

## VERSION

AW059628.1 GI:6651950

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 62)

Brenner, S., Williams, S.R., Vermaas, E.H., Storck, T., Moon, K.,

McCollum, C., Mao, J.I., Kirchner, J.J., Elettr, S., DuBridge, R.B.,

Burcham, T. and Albrecht, G.

In vitro cloning of complex mixtures of DNA on microbeads: Physical

separation of differentially expressed cDNAs

Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

20144098

10677516

Contact: Burcham TS

LYNX Therapeutics, Inc.

25861 Industrial Blvd., Hayward, CA 94545, USA

Tel: 510 670 9338

Fax: 510 670 9302

Email: timb@lynxgen.com

Sequence obtained from LYNX Therapeutics Megasort technology.

Collected from the down-regulated gate. Consensus sequence of 2

sequences in cluster.

High quality sequence stop: 62.

Location/Qualifiers

1..62

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/cell\_type="monocytic leukemia"

/cell\_line="THP-1 (TIB-202)"

/clone\_lib="DNC15"

/note="Vector: PCR2.1; Cloning of PCR products from

micro-beads carrying 3', end of down-regulated cDNA. THP-1

cells non-induced (treated with DMSO only)."

QY 3 RC 4

Db 62 RC 61

## ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 62;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RC 4

Db 62 RC 61

## RESULT 159

BES77741

LOCUS

DEFINITION

BES77741

EST011 Pigeon optic tecta cDNA library generated with SSH

methodology Columbia livia cDNA 5', mRNA sequence.

BES77741

ACCESSION

VERSION

BES77741.1 GI:9828687

KEYWORDS

SOURCE

ORGANISM

Columbia livia (domestic pigeon)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Columbiformes; Columba;

1 (bases 1 to 62)

Wang, Y., Xu, B. and Qi, M.

Differentially expressed genes in the pigeon optic tecta after

monocular deprivation

Unpublished (2001)

Contact: Wang, Y.

Molecular Biology

Tongji University School of Medicine

1238 Gonghexin Road, Shanghai, 200070, P. R. China

Tel: 021 6634 4540

Email: ywang@public2.sta.net.cn

Seq primer: T7

High quality sequence stop: 62

POLYA=No.

FEATURES source

Location/Qualifiers  
1. .62  
/organism="Columba livia"  
/mol\_type="mRNA"  
/db\_xref="taxon:9932"  
/tissue\_type="brain"  
/dev\_stage="adult"  
/clone\_lib="Pigeon optic tecta cDNA library generated with SSH methodology"  
/note="Vector: pBluescript(sk-); It was prepared with suppression subtractive hybridization (SSH).  
TAG\_TISSUE=Brain (Optic tecta)  
TAG\_SEQ=Not found"

ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 62;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WW 6  
||  
Db 18 WW 19

RESULT 160  
BE577741/c  
LOCUS  
DEFINITION EST011 Pigeon optic tecta cDNA library generated with SSH methodology  
ACCESSION BE577741  
VERSION BE577741.1 GI:9828687  
KEYWORDS EST.  
SOURCE  
ORGANISM  
Columba livia (domestic pigeon)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.  
REFERENCE  
1 (bases 1 to 62)  
Wang, Y., Xu, L. and Qi, M.  
Differentially expressed genes in the pigeon optic tecta after monocular deprivation  
Unpublished (2001)  
Contact: Wang, Y.  
Molecular Biology  
Tongji University School of Medicine  
1238 Gonghexin Road, Shanghai, 200070, P. R. China  
Tel: 021 6634 4540  
Email: ywange@public2.sta.net.cn  
Seq primer: T7  
High quality sequence stop: 62  
POLYA=No.

FEATURES source

Location/Qualifiers  
1. .62  
/organism="Columba livia"  
/mol\_type="mRNA"  
/db\_xref="taxon:9932"  
/tissue\_type="brain"  
/dev\_stage="adult"  
/clone\_lib="Pigeon optic tecta cDNA library generated with SSH methodology"  
/note="Vector: pBluescript(sk-); It was prepared with suppression subtractive hybridization (SSH).  
TAG\_TISSUE=Brain (Optic tecta)  
TAG\_SEQ=Not found"

RESULT 161  
AY433080  
LOCUS  
DEFINITION Aedes aegypti ASAP ID: 37497 unknown mRNA sequence.  
ACCESSION AY433080  
VERSION AY433080.1 GI:42761952  
KEYWORDS HTC.  
SOURCE  
Aedes aegypti (yellow fever mosquito)  
ORGANISM  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.  
REFERENCE  
1 (bases 1 to 62)  
Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.  
Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subalbatus  
Infect. Immun. 72 (7), 4114-4126 (2004)  
15213157  
2 (bases 1 to 62)  
Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Rusch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Kuo, H.-K., Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.  
Direct Submission  
Submitted (08-OCT-2003) Animal Health and Biomedical Sciences, University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI 53706, USA  
More information about this sequence is available in ASAP (A Systematic Annotation Package for community analysis of genomes) from the University of Wisconsin-Madison at  
<https://asap.ahabs.wisc.edu/annotation/php/logon.php>.

FEATURES source

Location/Qualifiers  
1. .62  
/organism="Aedes aegypti"  
/mol\_type="mRNA"  
/strain="liverpool"  
/isolation\_source="perfused hemolymph of bacteria-inoculated organisms at 1, 3, 6, 12, and 24 hours post-inoculation"  
/db\_xref="taxon:7159"  
/sex="female"  
/cell\_type="hemocyte"  
/tissue\_type="hemolymph"  
/dev\_stage="adult"  
/note="ASAP-UW Feature ID: 37496"

misc\_feature 1. .62  
/note="unknown; ASAP-UW Feature ID: 37497"

ORIGIN

Query Match 20.0%; Score 2; DB 3; Length 62;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5  
||  
Db 14 CW 15

RESULT 162  
AY433080/c  
LOCUS  
DEFINITION Aedes aegypti ASAP ID: 37497 unknown mRNA sequence.  
ACCESSION AY433080  
VERSION AY433080.1 GI:42761952  
KEYWORDS HTC.  
SOURCE  
Aedes aegypti (yellow fever mosquito)  
ORGANISM





JOURNAL Submitted (17-OCT-2003) Animal Health and Biomedical Sciences, University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI 53706, USA

COMMENT More information about this sequence is available in ASAP (A Systematic Annotation Package for community analysis of genomes) from the University of Wisconsin-Madison at <https://asap.ahabs.wisc.edu/annotation/php/logon.php>.

FEATURES  
source  
1..62  
/organism="Armigeres subalbatus"  
/mol\_type="mRNA"  
/isolation\_source="perfused hemolymph of bacteria-inoculated organisms at 1, 3, 6, 12, and 24 hours post-inoculation"  
/db\_xref="taxon:124917"  
/sex="female"  
/cell\_type="hemocyte"  
/tissue\_type="hemolymph"  
/dev\_stage="adult"  
/note="ASAP-UW Feature ID: 39226"  
misc\_feature  
1..62  
/note="unknown; low quality sequence; ASAP-UW Feature ID: 39227"

ORIGIN  
Query Match 20.0%; Score 2; DB 3; Length 62;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 5  
||  
54 CW 53

RESULT 165  
BQ704656  
LOCUS  
DEFINITION Bn01\_03h23 A 62 bp mRNA linear EST 16-JUL-2002  
Bn01\_AAPC\_ECORC transgenic Brassica napus overexpressing BNCBF17 co nstitutively\_frost\_tolerant Brassica napus cDNA clone Bn01\_03h23, mRNA sequence.

ACCESSION BQ704656  
VERSION BQ704656.1 GI:21844075  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
AUTHORS Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A., Chagnon, J., Farah, S., Couroux, P. and Hattori, J.  
TITLE Expressed Sequence Tags from constitutively frost tolerant transgenic Brassica napus overexpressing BNCBF17  
JOURNAL Unpublished (2002)  
COMMENT Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-food Canada  
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA 0C6, Canada  
Tel: (613) 759-1662  
Fax: (613) 759-1701  
Email: [singhja@agr.gc.ca](mailto:singhja@agr.gc.ca).

FEATURES  
source  
1..62  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Westar"  
/db\_xref="taxon:3708"  
/clone="Bn01\_03h23"  
/tissue\_type="fourth leaf"  
/dev\_stage="3 weeks seedling grown at room temperature"  
/clone\_lib="Bn01\_AAPC\_ECORC transgenic Brassica napus over expressing BNCBF17 constitutively frost tolerant"  
/note="vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Germinated in soil flats and seedlings grown for 3 weeks in a Conviron E-15 cabinet set at 20°C / 16 hr light (250 Em-2sec-1) and 16°C / 8 hr dark. Fourth leaves collected at 9 am and immediately frozen."

expressing BNCBF17 constitutively frost tolerant"  
/note="vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Germinated in soil flats and seedlings grown for 3 weeks in a Conviron E-15 cabinet set at 20°C / 16 hr light (250 Em-2sec-1) and 16°C / 8 hr dark. Fourth leaves collected at 9 am and immediately frozen."

ORIGIN  
Query Match 20.0%; Score 2; DB 5; Length 62;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 8  
||  
5 GY 6

RESULT 166  
BQ704656/c  
LOCUS  
DEFINITION Bn01\_03h23 A 62 bp mRNA linear EST 16-JUL-2002  
Bn01\_AAPC\_ECORC transgenic Brassica napus overexpressing BNCBF17 co nstitutively\_frost\_tolerant Brassica napus cDNA clone Bn01\_03h23, mRNA sequence.

ACCESSION BQ704656  
VERSION BQ704656.1 GI:21844075  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
AUTHORS Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A., Chagnon, J., Farah, S., Couroux, P. and Hattori, J.  
TITLE Expressed Sequence Tags from constitutively frost tolerant transgenic Brassica napus overexpressing BNCBF17  
JOURNAL Unpublished (2002)  
COMMENT Eastern Cereal and Oilseed Research Centre  
Agriculture and Agri-food Canada  
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA 0C6, Canada  
Tel: (613) 759-1662  
Fax: (613) 759-1701  
Email: [singhja@agr.gc.ca](mailto:singhja@agr.gc.ca).

FEATURES  
source  
1..62  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Westar"  
/db\_xref="taxon:3708"  
/clone="Bn01\_03h23"  
/tissue\_type="fourth leaf"  
/dev\_stage="3 weeks seedling grown at room temperature"  
/clone\_lib="Bn01\_AAPC\_ECORC transgenic Brassica napus over expressing BNCBF17 constitutively frost tolerant"  
/note="vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Germinated in soil flats and seedlings grown for 3 weeks in a Conviron E-15 cabinet set at 20°C / 16 hr light (250 Em-2sec-1) and 16°C / 8 hr dark. Fourth leaves collected at 9 am and immediately frozen."

ORIGIN  
Query Match 20.0%; Score 2; DB 5; Length 62;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RC 4  
||  
6 RC 5



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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR36E10"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 62;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CW 5
      ||
Db      49 CW 50

RESULT 170
CNS001GI/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC;
BACR36E10 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL074751.1 GI:4954531
VERSION
GSS.
KEYWORDS
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 62)
AUTHORS
Genoscope.
TITLES
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
Location/Qualifiers
1..62
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR36E10"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 62;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 WG 7
      ||
Db      50 WG 49

RESULT 171
CNS0119R
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN05E01 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL099993.1 GI:5611604
VERSION
GSS.
KEYWORDS
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 62)
AUTHORS
Genoscope.
TITLES
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CRPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES
Location/Qualifiers
1..62
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN05E01"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : T7"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 62;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GY 8
      ||
Db      22 GY 23

RESULT 172
CNS0119R/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN05E01 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL099993.1 GI:5611604
VERSION
GSS.
KEYWORDS
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 62)
AUTHORS
Genoscope.
TITLES
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CRPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

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```

FEATURES
  source
    Location/Qualifiers
      1. .62
        /organism="Drosophila melanogaster"
        /mol_type="genomic DNA"
        /db_xref="taxon:7227"
        /clone="BACN03E01"
        /clone_lib="DrosBAC"
        /plasmid="pBelOBAC11"
        /note="end : T7"

ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      3 RC 4
  DB      23 RC 22

RESULT 173
CNS02QCA
LOCUS
DEFINITION
  CNS02QCA
  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
  157D21 of library G from Tetraodon nigroviridis, genomic survey
  sequence.
ACCESSION
  AL209107
  AL209107.1 GI:7867926
KEYWORDS
  GSS; genome survey sequence.
SOURCE
  Tetraodon nigroviridis
  Tetraodon nigroviridis
  Tetraodon nigroviridis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
  Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
  Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE
  1
  Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
  Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
  Saurin, W. and Weissenbach, J.
  Estimate of human gene number provided by genome-wide analysis
  using Tetraodon nigroviridis DNA sequence
  Nat. Genet. 25 (2), 235-238 (2000)
  20296633
  PUBMED
  10835645
REFERENCE
  2
  Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
  Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
  Saurin, W., Bernot, A. and Weissenbach, J.
  Characterization and repeat analysis of the compact genome of the
  freshwater pufferfish Tetraodon nigroviridis
  Genome Res. 10 (7), 939-949 (2000)
  20359837
  PUBMED
  10899143
REFERENCE
  3 (bases 1 to 62)
  Genoscope.
  Direct Submission
  Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
  BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
  - Web : www.genoscope.cns.fr)
  This sequence is a single read and was generated as part of a large
  scale clone-end sequencing project of the Tetraodon nigroviridis
  genome. For more information, please take a look at
  http://www.genoscope.cns.fr/Tetraodon.
  Location/Qualifiers
    1. .62
      /organism="Tetraodon nigroviridis"
      /mol_type="genomic DNA"
      /db_xref="taxon:99883"
      /clone="157D21"
      /clone_lib="G"
      /note="Genoscope sequence ID : COAG157CB11SP1-end :
      PUC-Ori"

ORIGIN
  Query Match      20.0%; Score 2; DB 9; Length 62;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      6 WG 7
  DB      56 WG 55

FEATURES
  source
    Location/Qualifiers
      1. .62
        /organism="Drosophila melanogaster"
        /mol_type="genomic DNA"
        /db_xref="taxon:7227"
        /clone="BACN03E01"
        /clone_lib="DrosBAC"
        /plasmid="pBelOBAC11"
        /note="end : T7"

ORIGIN
  Query Match      20.0%; Score 2; DB 9; Length 62;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY      6 WG 7
  DB      56 WG 55

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RESULT 175
CNS04A3J
LOCUS      62 bp      DNA      linear      GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            09AD06 of library G from tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION  AL281368.1      GI:8019683
VERSION     AL281368.1
KEYWORDS   GSS; genome survey sequence.
SOURCE     Tetraodon nigroviridis
ORGANISM   Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE  1
AUTHORS    Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
TITLE      Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
JOURNAL    Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE    20296633
PUBMED     10835645
REFERENCE  2
AUTHORS    Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
TITLE      Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
JOURNAL    Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE    20296633
PUBMED     10835645
REFERENCE  3
AUTHORS    Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
TITLE      Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
JOURNAL    Genome Res. 10 (7), 939-949 (2000)
MEDLINE    20359837
PUBMED     10899143
REFERENCE  3 (bases 1 to 62)
AUTHORS    Genoscope.
TITLE      Direct Submission
JOURNAL    Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT    This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.

FEATURES   source
            Location/Qualifiers
            1..62
               /organism="Tetraodon nigroviridis"
               /mol_type="genomic DNA"
               /db_xref="taxon:99883"
               /clone="094D06"
               /clone_lib="G"
               /note="Genoscope sequence ID : C0BG094DB03SP1-end :
               PUC-Ori"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 62;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CW 5
        ||
Db      43 CW 42

RESULT 177
CNS04A3J
LOCUS      63 bp      mRNA      linear      EST 25-SEP-2000
DEFINITION AB555 Basidiome cDNA library Agaricus bisporus cDNA 5', mRNA
            sequence.
ACCESSION  AW444235
VERSION     AW444235.1      GI:10282033
KEYWORDS   EST.
SOURCE     Agaricus bisporus
ORGANISM   Agaricus bisporus
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
            Agaricales; Agaricaceae; Agaricus.

REFERENCE  1 (bases 1 to 63)
AUTHORS    Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Royse,D.J.
TITLE      Classification of sequences expressed during the primordial and
            basidiome stages of the cultivated mushroom Agaricus bisporus
JOURNAL    Fungal Genet. Biol. 29 (2), 81-94 (2000)
MEDLINE    20374017
PUBMED     10919377
COMMENT    Contact: Manuel D. Ospina-Giraldo

```

Mushroom Research Laboratory, Department of Plant Pathology  
The Pennsylvania State University  
305 Buckhout, University Park, PA 16802, USA  
Tel: 8148633073  
Fax: 8148637217  
Email: mxoll@psu.edu  
Seq primer: T7.

## FEATURES

source  
1. .63  
Location/Qualifiers  
/organism="Agaricus bisporus"  
/mol\_type="mRNA"  
/strain="Sylvan-130"  
/db\_xref="taxon:5341"  
/tissue\_type="Basidiome"  
/clone\_lib="Basidiome cDNA library"  
/note="Vector: pBluescript II SK (+); Site\_1: SalI;  
Site\_2: NotI"

## ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4  
||  
Db 28 RC 29

## RESULT 178

AW444235/c  
LOCUS  
DEFINITION  
AB555 Basidiome cDNA library Agaricus bisporus cDNA 5', mRNA  
EST.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Agaricus bisporus  
Agaricus bisporus  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
Agaricales; Agaricaceae; Agaricus.

REFERENCE  
AUTHORS  
TITLE  
Ospina-Giraldo, M.D., Collopy, P.D., Romaine, C.P. and Royse, D.J.  
Classification of sequences expressed during the primordial and  
basidiome stages of the cultivated mushroom Agaricus bisporus

Fungal Genet. Biol. 29 (2), 81-94 (2000)

JOURNAL  
MEDLINE  
PUBMED

20374017  
10919377

## COMMENT

Contact: Manuel D. Ospina-Giraldo  
Mushroom Research Laboratory, Department of Plant Pathology  
The Pennsylvania State University  
305 Buckhout, University Park, PA 16802, USA  
Tel: 8148633073  
Fax: 8148637217  
Email: mxoll@psu.edu  
Seq primer: T7.

## FEATURES

source  
1. .63  
Location/Qualifiers  
/organism="Agaricus bisporus"  
/mol\_type="mRNA"  
/strain="Sylvan-130"  
/db\_xref="taxon:5341"  
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/clone\_lib="Basidiome cDNA library"  
/note="Vector: pBluescript II SK (+); Site\_1: SalI;  
Site\_2: NotI"

## ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 8  
||

Db 29 GY 28

## RESULT 179

AW444251  
LOCUS  
DEFINITION  
AB015 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA  
EST.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Agaricus bisporus  
Agaricus bisporus  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
Agaricales; Agaricaceae; Agaricus.

REFERENCE  
AUTHORS  
TITLE  
Ospina-Giraldo, M.D., Collopy, P.D., Romaine, C.P. and Royse, D.J.  
Classification of sequences expressed during the primordial and  
basidiome stages of the cultivated mushroom Agaricus bisporus

Fungal Genet. Biol. 29 (2), 81-94 (2000)

JOURNAL  
MEDLINE  
PUBMED

20374017  
10919377

## COMMENT

Contact: Manuel D. Ospina-Giraldo  
Mushroom Research Laboratory, Department of Plant Pathology  
The Pennsylvania State University  
305 Buckhout, University Park, PA 16802, USA  
Tel: 8148633073  
Fax: 8148637217  
Email: mxoll@psu.edu  
Seq primer: T7.

## FEATURES

source  
1. .63  
Location/Qualifiers  
/organism="Agaricus bisporus"  
/mol\_type="mRNA"  
/strain="Sylvan-130"  
/db\_xref="taxon:5341"  
/tissue\_type="Primordium"  
/clone\_lib="Primordium cDNA library"  
/note="Vector: pBluescript II SK (+); Site\_1: SalI;  
Site\_2: NotI"

## ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7  
||  
Db 41 WG 42

## RESULT 180

AW444251/c  
LOCUS  
DEFINITION  
AB015 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA  
EST.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Agaricus bisporus  
Agaricus bisporus  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
Agaricales; Agaricaceae; Agaricus.

REFERENCE  
AUTHORS  
TITLE  
Ospina-Giraldo, M.D., Collopy, P.D., Romaine, C.P. and Royse, D.J.  
Classification of sequences expressed during the primordial and  
basidiome stages of the cultivated mushroom Agaricus bisporus

Fungal Genet. Biol. 29 (2), 81-94 (2000)

JOURNAL  
MEDLINE  
PUBMED

20374017  
10919377

## COMMENT

Contact: Manuel D. Ospina-Giraldo  
Mushroom Research Laboratory, Department of Plant Pathology  
The Pennsylvania State University

305 Buckhout, University Park, PA 16802, USA  
 Tel: 8148633073  
 Fax: 8148637217  
 Email: mxoll@psu.edu  
 Seq primer: 17.

#### FEATURES

source

Location/Qualifiers  
 1. .63  
 /organism="Agaricus bisporus"  
 /mol\_type="mRNA"  
 /strain="Sylvan-130"  
 /db\_xref="taxon:5341"  
 /tissue\_type="Primordium"  
 /clone\_lib="Primordium cDNA library"  
 /note="Vector: pBluescript II SK (+); Site\_1: SalI;  
 Site\_2: NotI"

#### ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5

Db 42 CW 41

#### RESULT 181

AY440539 AY440539 63 bp mRNA linear HTC 24-JUN-2004  
 LOCUS Armigeres subalbatus ASAP ID: 39257 unknown mRNA sequence.  
 DEFINITION  
 ACCESSION AY440539  
 VERSION AY440539.1 GI:42765568  
 KEYWORDS HTC.

#### SOURCE

ORGANISM Armigeres subalbatus  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
 Armigeres.  
 1 (bases 1 to 63)

REFERENCE 2 (bases 1 to 63)  
 AUTHORS Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,  
 Fuchs,J.F., Liss,P., Ruesch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,  
 Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,  
 Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and  
 Christensen,B.M.

TITLE Description of the Transcriptomes of Immune Response-Activated  
 Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres  
 subalbatus

JOURNAL Infect. Immun. 72 (7), 4114-4126 (2004)

PUBMED 15213157

#### REFERENCE

AUTHORS Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,  
 Liss,P., Ruesch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,  
 Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,  
 Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.

#### TITLE

JOURNAL Direct Submission  
 Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,  
 University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI  
 53706, USA

COMMENT More information about this sequence is available in ASAP (A  
 Systematic Annotation Package for community analysis of genomes)  
 from the University of Wisconsin-Madison at  
<https://asap.ahabs.wisc.edu/annotation/php/logon.php>.

#### FEATURES

source

Location/Qualifiers  
 1. .63  
 /organism="Armigeres subalbatus"  
 /mol\_type="mRNA"  
 /isolation\_source="perfused hemolymph of  
 bacteria-inoculated organisms at 1, 3, 6, 12, and 24  
 hours post-inoculation"  
 /db\_xref="taxon:124917"  
 /sex="female"  
 /cell\_type="hemocyte"  
 /tissue\_type="hemolymph"

/dev\_stage="adult"  
 /note="ASAP-UW Feature ID: 39256"  
 1. .63  
 /note="unknown; low quality sequence; ASAP-UW Feature ID:  
 39257"

#### misc\_feature

#### ORIGIN

Query Match 20.0%; Score 2; DB 3; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5

Db 23 CW 24

#### RESULT 182

AY440539/c AY440539 63 bp mRNA linear HTC 24-JUN-2004  
 LOCUS Armigeres subalbatus ASAP ID: 39257 unknown mRNA sequence.  
 DEFINITION  
 ACCESSION AY440539  
 VERSION AY440539.1 GI:42765568  
 KEYWORDS HTC.

#### SOURCE

ORGANISM Armigeres subalbatus  
 Armigeres subalbatus  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
 Armigeres.  
 1 (bases 1 to 63)

REFERENCE 2 (bases 1 to 63)  
 AUTHORS Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,  
 Fuchs,J.F., Liss,P., Ruesch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,  
 Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,  
 Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and  
 Christensen,B.M.

TITLE Description of the Transcriptomes of Immune Response-Activated  
 Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres  
 subalbatus

JOURNAL Infect. Immun. 72 (7), 4114-4126 (2004)

PUBMED 15213157

#### REFERENCE

AUTHORS Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,  
 Liss,P., Ruesch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,  
 Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,  
 Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.

#### TITLE

JOURNAL Direct Submission  
 Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,  
 University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI  
 53706, USA

COMMENT More information about this sequence is available in ASAP (A  
 Systematic Annotation Package for community analysis of genomes)  
 from the University of Wisconsin-Madison at  
<https://asap.ahabs.wisc.edu/annotation/php/logon.php>.

#### FEATURES

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Location/Qualifiers  
 1. .63  
 /organism="Armigeres subalbatus"  
 /mol\_type="mRNA"  
 /isolation\_source="perfused hemolymph of  
 bacteria-inoculated organisms at 1, 3, 6, 12, and 24  
 hours post-inoculation"  
 /db\_xref="taxon:124917"  
 /sex="female"  
 /cell\_type="hemocyte"  
 /tissue\_type="hemolymph"  
 /dev\_stage="adult"  
 /note="ASAP-UW Feature ID: 39256"  
 1. .63  
 /note="unknown; low quality sequence; ASAP-UW Feature ID:  
 39257"

#### misc\_feature

#### ORIGIN

Query Match 20.0%; Score 2; DB 3; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      6 WG 7
Db      24 WG 23

RESULT 183
BG838614
LOCUS
DEFINITION   Gc01_05d07_A_Gc01_AAPC_ECORC_cold_stressed_Glycine_clandestina
              63 bp mRNA linear EST 25-MAY-2001
              Glycine clandestina cDNA clone Gc01_05d07, mRNA sequence.
ACCESSION   BG838614
VERSION     BG838614.1 GI:14204936
KEYWORDS    EST.
SOURCE      Glycine clandestina
            Glycine clandestina
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
              Glycine.
REFERENCE   1 (bases 1 to 63)
AUTHORS    Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A.,
              Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and
              Tinker,N.A.
TITLE      Expressed Sequence Tags from Cold-Stressed Glycine clandestina
JOURNAL    Unpublished (2001)
COMMENT    Contact: Singh,J.A.
              Eastern Cereal and Oilseed Research Centre
              Agriculture and Agri-food Canada
              KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
              0C6, Canada
              Tel: (613) 759-1662
              Fax: (613) 759-1701
              Email: singhja@agr.gc.ca.
              Location/Qualifiers
              1..63
              /organism="Glycine clandestina"
              /mol_type="mRNA"
              /cultivar="1035"
              /db_xref="taxon:45687"
              /clone="Gc01_05d07"
              /tissue_type="Leaves, stem"
              /clone_lib="Gc01_AAPC_ECORC_cold_stressed_Glycine_clandest
              ina"
              /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
              Site 2: XhoI; Plants incubated at 2 degrees under 12 hours
              of light/day. Harvested after only 2-3 days of cold
              treatment. cDNA was prepared with the Uni-Zap cDNA kit
              from Stratagene. Eco RI adapters were linked followed by
              digest with Xho I/Eco RI and ligated to pBluescript."

FEATURES
source
1..63
/organism="Glycine clandestina"
/mol_type="mRNA"
/cultivar="1035"
/db_xref="taxon:45687"
/clone="Gc01_05d07"
/tissue_type="Leaves, stem"
/clone_lib="Gc01_AAPC_ECORC_cold_stressed_Glycine_clandest
ina"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
Site 2: XhoI; Plants incubated at 2 degrees under 12 hours
of light/day. Harvested after only 2-3 days of cold
treatment. cDNA was prepared with the Uni-Zap cDNA kit
from Stratagene. Eco RI adapters were linked followed by
digest with Xho I/Eco RI and ligated to pBluescript."

ORIGIN
Query Match      20.0%; Score 2; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GY 8
Db      35 GY 34

RESULT 185
CNS017GA
LOCUS
DEFINITION   Drosophila melanogaster genome survey sequence T7 end of BAC
              BACN17003 of DrosBAC library from Drosophila melanogaster (fruit
              fly), genomic survey sequence.
              63 bp DNA linear GSS 26-JUL-1999
ACCESSION   AL108004
VERSION     AL108004.1 GI:5628308
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
            Drosophila melanogaster
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Ephydroidea; Drosophilidae; Drosophila.
              1 (bases 1 to 63)
              Genoscope.
              Direct Submission
              Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
              BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
              - Web : www.genoscope.cns.fr)
              Determination of this BAC-end sequence was carried out as part of a
              collaboration with the European Drosophila Genome Project (EDGP) -
              http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
              library (Dros BAC) was made by Alain Billaud at CEPH (Centre
              d'Etude du Polymorphisme Humain) with funding provided by a MRC
              project grant. The DNA was prepared from embryos by Alain Bucheton
              and Genevieve Payan. It has been constructed in the vector
              pBelOBAC11.

REFERENCE   1 (bases 1 to 63)
AUTHORS    Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A.,
              Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and
              Tinker,N.A.
TITLE      Expressed Sequence Tags from Cold-Stressed Glycine clandestina
JOURNAL    Unpublished (2001)
COMMENT    Contact: Singh,J.A.
              Eastern Cereal and Oilseed Research Centre
              Agriculture and Agri-food Canada
              KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
              0C6, Canada
              Tel: (613) 759-1662
              Fax: (613) 759-1701
              Email: singhja@agr.gc.ca.
              Location/Qualifiers
              1..63
              /organism="Glycine clandestina"
              /mol_type="mRNA"
              /cultivar="1035"
              /db_xref="taxon:45687"
              /clone="Gc01_05d07"
              /tissue_type="Leaves, stem"
              /clone_lib="Gc01_AAPC_ECORC_cold_stressed_Glycine_clandest
              ina"
              /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
              Site 2: XhoI; Plants incubated at 2 degrees under 12 hours
              of light/day. Harvested after only 2-3 days of cold
              treatment. cDNA was prepared with the Uni-Zap cDNA kit
              from Stratagene. Eco RI adapters were linked followed by
              digest with Xho I/Eco RI and ligated to pBluescript."

ORIGIN
Query Match      20.0%; Score 2; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 RC 4
Db      34 RC 35

RESULT 184
BG838614/c
LOCUS
DEFINITION   Gc01_05d07_A_Gc01_AAPC_ECORC_cold_stressed_Glycine_clandestina
              63 bp mRNA linear EST 25-MAY-2001
              Glycine clandestina cDNA clone Gc01_05d07, mRNA sequence.
ACCESSION   BG838614
VERSION     BG838614.1 GI:14204936
KEYWORDS    EST.
SOURCE      Glycine clandestina
            Glycine clandestina
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```



[illegible]

```

REFERENCE
AUTHORS
1
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
MEDLINE
20296633
PUBMED
10835645
REFERENCE
AUTHORS
2
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL
MEDLINE
20359837
PUBMED
10899143
REFERENCE
AUTHORS
3 (bases 1 to 63)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1..63
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone_lib="198G06"
/clone_lib="G"
/notes="Genoscope sequence ID : COAG198BD03SP1-end :
PUC-ori"
ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 63;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7
||
Db 43 WG 42

RESULT 189
CNS02JW3
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
144G12 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION
AL200748
VERSION
AL200748.1 GI:7859093
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE
1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
MEDLINE
20296633
PUBMED
10835645
REFERENCE
2

```

```

AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL
MEDLINE
20359837
PUBMED
10899143
REFERENCE
AUTHORS
3 (bases 1 to 63)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1..63
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone_lib="144G12"
/clone_lib="G"
/notes="Genoscope sequence ID : COAG144BD06LP1-end : T7"
ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 63;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7
||
Db 34 WG 35

RESULT 190
CNS02JW3/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
144G12 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION
AL200748
VERSION
AL200748.1 GI:7859093
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE
1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
MEDLINE
20359837
PUBMED
10835645
REFERENCE
2
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL
MEDLINE
20359837
PUBMED
10899143
REFERENCE
AUTHORS
3 (bases 1 to 63)
Genoscope.
Direct Submission

```

**JOURNAL** Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)

**COMMENT** This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

**FEATURES** Location/Qualifiers  
 source  
 1. .63  
 /organism="Tetraodon nigroviridis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:99883"  
 /clone\_lib="G"  
 /note="Genoscope sequence ID : COAG144BD06LPI-end : T7"

**ORIGIN**

Query Match 20.0%; Score 2; DB 9; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5  
 ||  
 Db 35 CW 34

**RESULT 191**

**CNS02PAK**

**LOCUS** CNS02PAK 63 bp DNA linear GSS 01-SEP-2000

**DEFINITION** Tetraodon nigroviridis genome survey sequence T7 end of clone 155M16 of library G from Tetraodon nigroviridis, genomic survey sequence.

**ACCESSION** AL207749

**VERSION** AL207749.1 GI:7866568

**KEYWORDS** GSS; genome survey sequence.

**SOURCE** Tetraodon nigroviridis

**ORGANISM** Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

**REFERENCE** 1  
**AUTHORS** Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.  
 Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
 Nat. Genet. 25 (2), 235-238 (2000)

**TITLE** Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence

**JOURNAL** Nat. Genet. 25 (2), 235-238 (2000)

**MEDLINE** 20296633

**PUBMED** 10835645

**REFERENCE** 2  
**AUTHORS** Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Fizames,C., Fischer,C., Bernot,A., Wincker,P., Brottier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
 Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
 Genome Res. 10 (7), 939-949 (2000)

**TITLE** Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

**JOURNAL** Genome Res. 10 (7), 939-949 (2000)

**MEDLINE** 20359837

**PUBMED** 10899143

**REFERENCE** 3 (bases 1 to 63)  
**AUTHORS** Genoscope.  
 Direct Submission

**TITLE** Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)

**JOURNAL** BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)

**COMMENT** This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

**FEATURES** Location/Qualifiers  
 source  
 1. .63  
 /organism="Tetraodon nigroviridis"  
 /mol\_type="genomic DNA"

**ORIGIN**

Query Match 20.0%; Score 2; DB 9; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7  
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 Db 52 WG 53

**RESULT 192**

**CNS02PAK/c**

**LOCUS** CNS02PAK 63 bp DNA linear GSS 01-SEP-2000

**DEFINITION** Tetraodon nigroviridis genome survey sequence T7 end of clone 155M16 of library G from Tetraodon nigroviridis, genomic survey sequence.

**ACCESSION** AL207749

**VERSION** AL207749.1 GI:7866568

**KEYWORDS** GSS; genome survey sequence.

**SOURCE** Tetraodon nigroviridis

**ORGANISM** Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

**REFERENCE** 1  
**AUTHORS** Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.  
 Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
 Nat. Genet. 25 (2), 235-238 (2000)

**TITLE** Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence

**JOURNAL** Nat. Genet. 25 (2), 235-238 (2000)

**MEDLINE** 20296633

**PUBMED** 10835645

**REFERENCE** 2  
**AUTHORS** Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Fizames,C., Fischer,C., Bernot,A., Wincker,P., Brottier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
 Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
 Genome Res. 10 (7), 939-949 (2000)

**TITLE** Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

**JOURNAL** Genome Res. 10 (7), 939-949 (2000)

**MEDLINE** 20359837

**PUBMED** 10899143

**REFERENCE** 3 (bases 1 to 63)  
**AUTHORS** Genoscope.  
 Direct Submission

**TITLE** Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)

**JOURNAL** BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)

**COMMENT** This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

**FEATURES** Location/Qualifiers  
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 1. .63  
 /organism="Tetraodon nigroviridis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:99883"  
 /clone\_lib="G"  
 /note="Genoscope sequence ID : COAG155BG08LPI-end : T7"

**ORIGIN**

Query Match 20.0%; Score 2; DB 9; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5

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Db          53 CW 52

RESULT 193
CNS03SXE
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
054J01 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION
AL259115.1
VERSION
AL259115.1 GI:7980127
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE
20296633
PUBMED
10835645
REFERENCE
2
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
TITLE
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL
Genome Res. 10 (7), 939-949 (2000)
MEDLINE
20359837
PUBMED
10899143
REFERENCE
3 (bases 1 to 63)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source
1..63
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="054J01"
/clone_lib="G"
/note="Genoscope sequence ID : COBG054CE01LP1-end : T7"

ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 63;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WG 7
Db 31 WG 30

RESULT 195
CNS04DE2
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
102G10 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL285635
VERSION
AL285635.1 GI:8024061
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,

```

**TITLE**  
Saurin,W. and Weissenbach,J.  
Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence  
Nat. Genet. 25 (2), 235-238 (2000)

**JOURNAL**  
MEDLINE  
PUBMED  
20296633  
REFERENCE  
2  
10835645  
AUTHORS

**TITLE**  
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,  
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,P.,  
Saurin,W., Bernot,A. and Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Genome Res. 10 (7), 939-949 (2000)

**JOURNAL**  
MEDLINE  
PUBMED  
20359837  
REFERENCE  
3 (bases 1 to 63)  
AUTHORS  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetraodon.

**FEATURES**  
source  
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/mol\_type="genomic DNA"  
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/note="Genoscope sequence ID : COBG102BD05SP1-end :  
PUC-Ori"

**ORIGIN**  
Query Match 20.0%; Score 2; DB 9; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 CW 5  
||  
Db 43 CW 44

**RESULT 196**  
CNS04DE2/c  
LOCUS  
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
102G10 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
AL285635  
VERSION AL285635.1 GI:8024061  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetraodon nigroviridis  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;  
Tetraodontidae; Tetraodontidae; Tetraodon.  
1  
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,P.,  
Saurin,W. and Weissenbach,J.  
Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence  
Nat. Genet. 25 (2), 235-238 (2000)

**JOURNAL**  
MEDLINE  
PUBMED  
20296633  
REFERENCE  
2  
10835645  
AUTHORS

**TITLE**  
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,  
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,P.,  
Saurin,W., Bernot,A. and Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Genome Res. 10 (7), 939-949 (2000)

**JOURNAL**  
MEDLINE  
PUBMED  
20359837  
REFERENCE  
3 (bases 1 to 63)  
AUTHORS  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetraodon.

**FEATURES**  
source  
1..63  
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PUC-Ori"

**ORIGIN**  
Query Match 20.0%; Score 2; DB 9; Length 63;  
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 CW 5  
||  
Db 43 CW 44

**RESULT 197**  
R28845  
LOCUS  
F1-6D 22 week old human fetal liver cDNA library Homo sapiens cDNA  
clone F1-6D 5', mRNA sequence.  
R28845  
ACCESSION R28845.1 GI:6514217  
VERSION R28845  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 64)  
Choi,S., Yun,J.W., Choi,E.K., Cho,Y.G., Sung,Y.C. and Shin,H.S.  
Construction of a gene expression profile of a human fetal liver by  
single-pass cDNA sequencing  
Mamm. Genome 6 (9), 653-657 (1995)  
96081342  
MEDLINE  
PUBMED  
8535075  
COMMENT  
Contact: Hee-Sup Shin  
Developmental Genetics  
Pohang Institute of Science & Technology  
San31 Hyejodong Pohang, 790-784 Republic of Korea  
Tel: 562-279-2291  
Fax: 562-279-2199  
Email: shinhs@vision.postech.ac.kr  
Seq primer: T3 primer.  
Location/Qualifiers  
1..64  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="F1-6D"  
/lab\_host="XLI-blue MRF"  
/clone\_lib="22 week old human fetal liver cDNA library"  
/note="vector: pBluescriptII SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; The cDNA library made by oligo-dT primed and  
directionally cloned between 5'ExoR I-XhoI3' sites."

**TITLE**  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Genome Res. 10 (7), 939-949 (2000)

**JOURNAL**  
MEDLINE  
PUBMED  
20359837  
REFERENCE  
3 (bases 1 to 63)  
AUTHORS  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/Tetraodon.

**FEATURES**  
source  
1..63  
/organism="Tetraodon nigroviridis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:99883"  
/clone="102G10"  
/clone\_lib="G"  
/note="Genoscope sequence ID : COBG102BD05SP1-end :  
PUC-Ori"

**ORIGIN**  
Query Match 20.0%; Score 2; DB 9; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 WG 7  
||  
Db 44 WG 43

**RESULT 197**  
R28845  
LOCUS  
F1-6D 22 week old human fetal liver cDNA library Homo sapiens cDNA  
clone F1-6D 5', mRNA sequence.  
R28845  
ACCESSION R28845.1 GI:6514217  
VERSION R28845  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 64)  
Choi,S., Yun,J.W., Choi,E.K., Cho,Y.G., Sung,Y.C. and Shin,H.S.  
Construction of a gene expression profile of a human fetal liver by  
single-pass cDNA sequencing  
Mamm. Genome 6 (9), 653-657 (1995)  
96081342  
MEDLINE  
PUBMED  
8535075  
COMMENT  
Contact: Hee-Sup Shin  
Developmental Genetics  
Pohang Institute of Science & Technology  
San31 Hyejodong Pohang, 790-784 Republic of Korea  
Tel: 562-279-2291  
Fax: 562-279-2199  
Email: shinhs@vision.postech.ac.kr  
Seq primer: T3 primer.  
Location/Qualifiers  
1..64  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="F1-6D"  
/lab\_host="XLI-blue MRF"  
/clone\_lib="22 week old human fetal liver cDNA library"  
/note="vector: pBluescriptII SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; The cDNA library made by oligo-dT primed and  
directionally cloned between 5'ExoR I-XhoI3' sites."

## ORIGIN

Query Match 20.0%; Score 2; DB 7; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 5  
 ||  
 1 CW 2

Db

## RESULT 198

R28845/c  
 LOCUS  
 DEFINITION F1-6D 22 week old human fetal liver cDNA library Homo sapiens cDNA  
 clone F1-6D 5', mRNA sequence.

## ACCESSION

R28845 64 bp mRNA linear EST 03-DEC-1999

## VERSION

R28845.1 GI:6514217

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 64)  
 Choi,S.S., Yun,J.W., Choi,E.K., Cho,Y.G., Sung,Y.C. and Shin,H.S.  
 Construction of a gene expression profile of a human fetal liver by  
 single-pass cDNA sequencing  
 Mamm. Genome 6 (9), 653-657 (1995)  
 96081342  
 8535075  
 Contact: Hee-Sup Shin  
 Developmental Genetics  
 Pohang Institute of Science & Technology  
 San31, Hyodong Pohang, 790-784 Republic of Korea  
 Tel: 562-279-2291  
 Fax: 562-279-2199  
 Email: shinh@vision.postech.ac.kr  
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 Location/Qualifiers  
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## FEATURES

source

## ORIGIN

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## RESULT 199

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 LOCUS  
 DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #  
 BACR27L06 of RPCI-98 library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.

## ACCESSION

AL060631 GI:4947791

## KEYWORDS

GSS.

## SOURCE

Drosophila melanogaster (fruit fly)  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 64)  
 Genoscope.  
 Direct Submission  
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aaron Mammose in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's  
 P1 and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be  
 found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

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## RESULT 200

## LOCUS

## DEFINITION

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 BACR27L06 of RPCI-98 library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.

## ACCESSION

AL060631 GI:4947791

## KEYWORDS

## SOURCE

## ORGANISM

Drosophila melanogaster (fruit fly)  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Direct Submission  
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aaron Mammose in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's  
 P1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

Location/Qualifiers

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Qy 7 GY 8

Db 58 GY 57

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Job time : 2736 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 16:25:29 ; Search time 82 Seconds  
(without alignments)  
86.682 Million cell updates/sec

Title: US-09-813-824A-3  
Perfect score: 10  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 35539441 residues

Word size : 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
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#### SUMMARIES

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c 149	3	30.0	13	1	US-08-235-503B-33	Sequence 33, Appl	c 222	3	30.0	17	4	US-09-564-595D-10	Sequence 10, Appl
c 150	3	30.0	13	1	US-08-235-503B-33	Sequence 33, Appl	c 223	3	30.0	17	4	US-09-564-595D-10	Sequence 10, Appl
c 151	3	30.0	13	1	US-08-643-886-3	Sequence 3, Appl	c 224	3	30.0	17	4	US-09-706-968-10	Sequence 10, Appl
c 152	3	30.0	13	1	US-08-643-886-3	Sequence 3, Appl	c 225	3	30.0	17	4	US-09-706-968-10	Sequence 10, Appl
c 153	3	30.0	13	1	US-08-643-886-3	Sequence 3, Appl	c 226	3	30.0	17	4	US-09-132-368-28	Sequence 28, Appl
c 154	3	30.0	13	1	US-08-643-886-15	Sequence 15, Appl	c 227	3	30.0	17	4	US-09-132-368-28	Sequence 28, Appl
c 155	3	30.0	13	5	PCT-US95-05265-33	Sequence 33, Appl	c 228	3	30.0	17	4	US-09-250-124A-16	Sequence 16, Appl
c 156	3	30.0	13	5	PCT-US95-05265-33	Sequence 33, Appl	c 229	3	30.0	17	4	US-09-250-124A-16	Sequence 16, Appl
c 157	3	30.0	14	1	US-07-882-838E-32	Sequence 32, Appl	c 230	3	30.0	17	4	US-10-043-142-1	Sequence 1, Appl
c 158	3	30.0	14	1	US-07-882-838E-32	Sequence 32, Appl	c 231	3	30.0	17	4	US-10-043-142-1	Sequence 1, Appl
c 159	3	30.0	14	1	US-08-643-886-4	Sequence 4, Appl	c 232	3	30.0	17	4	US-09-806-399-1	Sequence 1, Appl
c 160	3	30.0	14	1	US-08-643-886-4	Sequence 4, Appl	c 233	3	30.0	17	4	US-09-806-399-1	Sequence 1, Appl
c 161	3	30.0	14	1	US-08-643-886-16	Sequence 16, Appl	c 234	3	30.0	17	4	US-09-545-894-18	Sequence 18, Appl
c 162	3	30.0	14	1	US-08-643-886-16	Sequence 16, Appl	c 235	3	30.0	17	4	US-09-545-894-18	Sequence 18, Appl
c 163	3	30.0	14	3	US-08-646-789A-38	Sequence 38, Appl	c 236	3	30.0	17	4	US-09-545-894-19	Sequence 19, Appl
c 164	3	30.0	14	3	US-08-646-789A-38	Sequence 38, Appl	c 237	3	30.0	17	4	US-09-545-894-19	Sequence 19, Appl
c 165	3	30.0	14	3	US-08-646-789A-39	Sequence 39, Appl	c 238	3	30.0	18	1	US-08-643-886-8	Sequence 8, Appl
c 166	3	30.0	14	3	US-08-646-789A-39	Sequence 39, Appl	c 239	3	30.0	18	1	US-08-643-886-8	Sequence 8, Appl
c 167	3	30.0	14	3	US-08-646-301A-8	Sequence 8, Appl	c 240	3	30.0	18	1	US-08-643-886-20	Sequence 20, Appl
c 168	3	30.0	14	3	US-08-646-301A-8	Sequence 8, Appl	c 241	3	30.0	18	1	US-08-643-886-20	Sequence 20, Appl
c 169	3	30.0	14	3	US-09-305-639-7	Sequence 7, Appl	c 242	3	30.0	18	3	US-09-040-025-21	Sequence 21, Appl
c 170	3	30.0	14	3	US-09-305-639-7	Sequence 7, Appl	c 243	3	30.0	18	3	US-09-040-025-21	Sequence 21, Appl
c 171	3	30.0	14	3	US-09-305-384-8	Sequence 8, Appl	c 244	3	30.0	18	3	US-09-040-025-21	Sequence 21, Appl
c 172	3	30.0	14	3	US-09-305-384-8	Sequence 8, Appl	c 245	3	30.0	19	1	US-08-474-542A-136	Sequence 136, App
c 173	3	30.0	14	4	US-09-318-138-22	Sequence 22, Appl	c 246	3	30.0	19	1	US-08-474-542A-136	Sequence 136, App

c 247	3	30.0	19	1	US-08-235-503B-10	Sequence 10, Appl	c 320	3	30.0	23	3	US-09-446-504-48	Sequence 48, Appl
c 248	3	30.0	19	1	US-08-235-503B-11	Sequence 10, Appl	321	3	30.0	23	3	US-09-040-025-62	Sequence 62, Appl
c 249	3	30.0	19	1	US-08-235-503B-10	Sequence 11, Appl	c 322	3	30.0	23	3	US-09-040-025-62	Sequence 62, Appl
c 250	3	30.0	19	1	US-08-235-503B-11	Sequence 11, Appl	323	3	30.0	23	3	US-09-040-025-64	Sequence 64, Appl
c 251	3	30.0	19	1	US-07-882-838E-10	Sequence 10, Appl	c 324	3	30.0	23	3	US-09-040-025-64	Sequence 64, Appl
c 252	3	30.0	19	1	US-07-882-838E-10	Sequence 10, Appl	325	3	30.0	23	3	US-09-712-266-48	Sequence 48, Appl
c 253	3	30.0	19	1	US-08-457-648-136	Sequence 136, App	c 326	3	30.0	23	3	US-09-712-266-48	Sequence 48, Appl
c 254	3	30.0	19	1	US-08-457-648-136	Sequence 136, App	327	3	30.0	23	3	US-08-513-974B-15	Sequence 15, Appl
c 255	3	30.0	19	1	US-08-643-886-9	Sequence 9, Appl	c 328	3	30.0	24	3	US-08-513-974B-15	Sequence 15, Appl
c 256	3	30.0	19	1	US-08-643-886-9	Sequence 9, Appl	329	3	30.0	24	3	US-08-513-974B-230	Sequence 230, App
c 257	3	30.0	19	4	US-09-672-717-209	Sequence 209, App	c 330	3	30.0	24	3	US-08-513-974B-230	Sequence 230, App
c 258	3	30.0	19	4	US-09-672-717-209	Sequence 209, App	331	3	30.0	24	4	US-09-461-436B-15	Sequence 15, Appl
c 259	3	30.0	19	4	US-09-672-717-211	Sequence 211, App	c 332	3	30.0	24	4	US-09-461-436B-15	Sequence 15, Appl
c 260	3	30.0	19	4	US-09-672-717-211	Sequence 211, App	333	3	30.0	24	4	US-09-418-980-78	Sequence 78, Appl
c 261	3	30.0	19	5	PCT-US95-05265-10	Sequence 10, Appl	c 334	3	30.0	24	4	US-09-418-980-78	Sequence 78, Appl
c 262	3	30.0	19	5	PCT-US95-05265-10	Sequence 10, Appl	335	3	30.0	25	1	US-07-959-119A-7	Sequence 7, Appl
c 263	3	30.0	19	5	PCT-US95-05265-11	Sequence 11, Appl	c 336	3	30.0	25	1	US-07-959-119A-7	Sequence 7, Appl
c 264	3	30.0	19	5	PCT-US95-05265-11	Sequence 11, Appl	337	3	30.0	25	1	US-08-744-722-1	Sequence 1, Appl
c 265	3	30.0	20	1	US-07-940-242A-5	Sequence 5, Appl	c 338	3	30.0	25	2	US-08-744-722-1	Sequence 1, Appl
c 266	3	30.0	20	1	US-07-940-242A-5	Sequence 5, Appl	339	3	30.0	25	2	US-08-471-994-6	Sequence 6, Appl
c 267	3	30.0	20	1	US-07-940-242A-7	Sequence 7, Appl	c 340	3	30.0	25	2	US-08-471-994-6	Sequence 6, Appl
c 268	3	30.0	20	1	US-07-940-242A-7	Sequence 7, Appl	341	3	30.0	25	3	US-08-471-994-6	Sequence 6, Appl
c 269	3	30.0	20	1	US-08-474-542A-130	Sequence 130, App	c 342	3	30.0	25	3	US-08-979-917A-15	Sequence 15, Appl
c 270	3	30.0	20	1	US-08-474-542A-130	Sequence 130, App	343	3	30.0	25	3	US-08-979-917A-15	Sequence 15, Appl
c 271	3	30.0	20	1	US-08-457-648-130	Sequence 130, App	c 344	3	30.0	25	4	US-09-743-954-4	Sequence 4, Appl
c 272	3	30.0	20	1	US-08-457-648-130	Sequence 130, App	345	3	30.0	25	4	US-09-743-954-4	Sequence 4, Appl
c 273	3	30.0	20	1	US-08-643-886-10	Sequence 10, Appl	c 346	3	30.0	25	4	US-08-397-335-7	Sequence 7, Appl
c 274	3	30.0	20	1	US-08-643-886-10	Sequence 10, Appl	347	3	30.0	25	4	US-08-397-335-7	Sequence 7, Appl
c 275	3	30.0	20	2	US-08-680-326-126	Sequence 126, App	c 348	3	30.0	26	1	US-07-714-131C-343	Sequence 343, App
c 276	3	30.0	20	2	US-08-680-326-126	Sequence 126, App	349	3	30.0	26	1	US-07-714-131C-343	Sequence 343, App
c 277	3	30.0	20	4	US-09-132-368-30	Sequence 30, Appl	c 350	3	30.0	26	1	US-07-959-119A-10	Sequence 10, Appl
c 278	3	30.0	20	4	US-09-132-368-30	Sequence 30, Appl	351	3	30.0	26	1	US-07-959-119A-10	Sequence 10, Appl
c 279	3	30.0	20	4	US-09-732-615-19	Sequence 19, Appl	c 352	3	30.0	26	1	US-08-412-110-343	Sequence 343, App
c 280	3	30.0	20	4	US-09-732-615-19	Sequence 19, Appl	353	3	30.0	26	1	US-08-412-110-343	Sequence 343, App
c 281	3	30.0	20	4	US-10-273-051-19	Sequence 19, Appl	c 354	3	30.0	26	1	US-08-409-442A-343	Sequence 343, App
c 282	3	30.0	21	1	US-08-474-542A-298	Sequence 298, App	355	3	30.0	26	2	US-08-409-442A-343	Sequence 343, App
c 283	3	30.0	21	1	US-08-474-542A-298	Sequence 298, App	c 356	3	30.0	26	2	US-08-469-609A-343	Sequence 343, App
c 284	3	30.0	21	1	US-08-457-648-298	Sequence 298, App	357	3	30.0	26	2	US-08-469-609A-343	Sequence 343, App
c 285	3	30.0	21	1	US-08-457-648-298	Sequence 298, App	c 358	3	30.0	26	2	US-08-680-326-5	Sequence 5, Appl
c 286	3	30.0	21	1	US-08-457-648-298	Sequence 298, App	359	3	30.0	26	2	US-08-680-326-5	Sequence 5, Appl
c 287	3	30.0	21	2	US-08-632-598-10	Sequence 10, Appl	c 360	3	30.0	26	2	US-08-680-326-6	Sequence 6, Appl
c 288	3	30.0	21	2	US-08-632-598-10	Sequence 10, Appl	361	3	30.0	26	2	US-08-680-326-6	Sequence 6, Appl
c 289	3	30.0	21	3	US-09-040-025-76	Sequence 76, Appl	c 362	3	30.0	26	3	US-08-906-443-2	Sequence 2, Appl
c 290	3	30.0	21	3	US-09-040-025-76	Sequence 76, Appl	363	3	30.0	26	3	US-08-906-443-2	Sequence 2, Appl
c 291	3	30.0	21	3	US-09-040-025-78	Sequence 78, Appl	c 364	3	30.0	26	3	US-09-143-190-343	Sequence 343, App
c 292	3	30.0	21	3	US-09-040-025-78	Sequence 78, Appl	365	3	30.0	26	3	US-09-143-190-343	Sequence 343, App
c 293	3	30.0	21	3	US-09-040-025-107	Sequence 107, App	c 366	3	30.0	26	3	US-08-154-364-13	Sequence 13, Appl
c 294	3	30.0	21	3	US-09-040-025-107	Sequence 107, App	367	3	30.0	26	3	US-08-154-364-13	Sequence 13, Appl
c 295	3	30.0	21	3	US-09-040-025-109	Sequence 109, App	c 368	3	30.0	26	3	US-08-973-124-269	Sequence 269, App
c 296	3	30.0	21	3	US-09-040-025-109	Sequence 109, App	369	3	30.0	26	3	US-08-973-124-269	Sequence 269, App
c 297	3	30.0	21	3	US-09-231-240-10	Sequence 10, Appl	c 370	3	30.0	26	3	US-09-502-344-343	Sequence 343, App
c 298	3	30.0	21	3	US-09-231-240-10	Sequence 10, Appl	371	3	30.0	26	4	US-09-502-344-343	Sequence 343, App
c 299	3	30.0	21	3	US-09-040-025-76	Sequence 76, Appl	c 372	3	30.0	26	4	US-08-397-335-10	Sequence 10, Appl
c 300	3	30.0	21	3	US-09-040-025-76	Sequence 76, Appl	373	3	30.0	26	5	US-08-397-335-10	Sequence 10, Appl
c 301	3	30.0	21	3	US-09-040-025-78	Sequence 78, Appl	c 374	3	30.0	26	5	PCT-US96-08014-269	Sequence 269, App
c 302	3	30.0	21	3	US-09-040-025-78	Sequence 78, Appl	375	3	30.0	26	5	PCT-US96-08014-269	Sequence 269, App
c 303	3	30.0	21	3	US-09-040-025-107	Sequence 107, App	c 376	3	30.0	27	1	US-07-714-131C-337	Sequence 337, App
c 304	3	30.0	21	3	US-09-040-025-107	Sequence 107, App	377	3	30.0	27	1	US-07-714-131C-337	Sequence 337, App
c 305	3	30.0	21	3	US-09-040-025-109	Sequence 109, App	c 378	3	30.0	27	1	US-08-412-110-337	Sequence 337, App
c 306	3	30.0	21	3	US-09-040-025-109	Sequence 109, App	379	3	30.0	27	1	US-08-412-110-337	Sequence 337, App
c 307	3	30.0	22	3	US-08-213-741-10	Sequence 10, Appl	c 380	3	30.0	27	1	US-08-409-442A-337	Sequence 337, App
c 308	3	30.0	22	3	US-08-213-741-10	Sequence 10, Appl	381	3	30.0	27	1	US-08-409-442A-337	Sequence 337, App
c 309	3	30.0	22	3	US-08-522-336-10	Sequence 10, Appl	c 382	3	30.0	27	2	US-08-469-609A-337	Sequence 337, App
c 310	3	30.0	22	3	US-08-522-336-10	Sequence 10, Appl	383	3	30.0	27	2	US-08-469-609A-337	Sequence 337, App
c 311	3	30.0	23	2	US-08-199-984-3	Sequence 3, Appl	c 384	3	30.0	27	3	US-09-143-190-337	Sequence 337, App
c 312	3	30.0	23	2	US-08-199-984-3	Sequence 3, Appl	385	3	30.0	27	3	US-09-143-190-337	Sequence 337, App
c 313	3	30.0	23	2	US-08-896-365-21	Sequence 21, Appl	c 386	3	30.0	27	3	US-08-709-838-4	Sequence 4, Appl
c 314	3	30.0	23	2	US-08-896-365-21	Sequence 21, Appl	387	3	30.0	27	3	US-08-709-838-4	Sequence 4, Appl
c 315	3	30.0	23	3	US-09-040-025-62	Sequence 62, Appl	c 388	3	30.0	27	3	US-08-829-839-4	Sequence 4, Appl
c 316	3	30.0	23	3	US-09-040-025-62	Sequence 62, Appl	389	3	30.0	27	3	US-08-829-839-4	Sequence 4, Appl
c 317	3	30.0	23	3	US-09-040-025-64	Sequence 64, Appl	c 390	3	30.0	27	3	US-08-154-364-6	Sequence 6, Appl
c 318	3	30.0	23	3	US-09-040-025-64	Sequence 64, Appl	391	3	30.0	27	3	US-08-154-364-6	Sequence 6, Appl
c 319	3	30.0	23	3	US-09-446-504-48	Sequence 48, Appl	c 392	3	30.0	27	3	US-08-973-124-268	Sequence 268, App

393	3	30.0	27	3	US-09-502-344-337	Sequence 337, App	C 466	3	30.0	33	3	US-08-441-971-81	Sequence 81, Appl
394	3	30.0	27	3	US-09-502-344-337	Sequence 337, App	467	3	30.0	33	3	US-08-441-971-100	Sequence 100, App
395	3	30.0	27	4	US-08-403-459-59	Sequence 59, Appl	C 468	3	30.0	33	3	US-08-441-971-100	Sequence 100, App
396	3	30.0	27	4	US-08-403-459-59	Sequence 59, Appl	469	3	30.0	33	3	US-08-441-971-103	Sequence 103, App
397	3	30.0	27	4	US-08-403-459-60	Sequence 60, Appl	C 470	3	30.0	33	3	US-08-441-971-103	Sequence 103, App
398	3	30.0	27	4	US-08-403-459-60	Sequence 60, Appl	C 471	3	30.0	33	3	US-08-441-971-113	Sequence 113, App
399	3	30.0	27	4	US-09-033-936-52	Sequence 52, Appl	C 472	3	30.0	33	3	US-08-441-971-113	Sequence 113, App
400	3	30.0	27	4	US-09-033-936-52	Sequence 52, Appl	C 473	3	30.0	33	3	US-08-467-023-104	Sequence 104, App
401	3	30.0	27	4	US-09-684-579-9	Sequence 9, Appl	C 474	3	30.0	33	3	US-08-467-023-104	Sequence 104, App
402	3	30.0	27	4	US-09-684-579-9	Sequence 9, Appl	C 475	3	30.0	33	3	US-08-451-374-11	Sequence 11, Appl
403	3	30.0	27	4	US-09-624-594-4	Sequence 4, Appl	C 476	3	30.0	33	3	US-08-451-374-11	Sequence 11, Appl
404	3	30.0	27	4	US-09-624-594-4	Sequence 4, Appl	C 477	3	30.0	33	3	US-08-221-653-81	Sequence 81, Appl
405	3	30.0	27	5	PCT-US96-08014-268	Sequence 268, App	C 478	3	30.0	33	3	US-08-221-653-81	Sequence 81, Appl
406	3	30.0	27	5	PCT-US96-08014-268	Sequence 268, App	C 479	3	30.0	33	3	US-08-221-653-100	Sequence 100, App
407	3	30.0	28	1	US-07-752-101A-32	Sequence 32, Appl	C 480	3	30.0	33	3	US-08-221-653-100	Sequence 100, App
408	3	30.0	28	1	US-07-752-101A-32	Sequence 32, Appl	C 481	3	30.0	33	3	US-08-221-653-103	Sequence 103, App
409	3	30.0	29	1	US-07-714-131C-342	Sequence 342, App	C 482	3	30.0	33	3	US-08-221-653-103	Sequence 103, App
410	3	30.0	29	1	US-07-714-131C-342	Sequence 342, App	C 483	3	30.0	33	3	US-08-221-653-113	Sequence 113, App
411	3	30.0	29	1	US-08-275-225-25	Sequence 25, Appl	C 484	3	30.0	33	3	US-08-221-653-113	Sequence 113, App
412	3	30.0	29	1	US-08-275-225-25	Sequence 25, Appl	C 485	3	30.0	33	3	US-08-442-144A-81	Sequence 81, Appl
413	3	30.0	29	1	US-08-412-110-342	Sequence 342, App	C 486	3	30.0	33	3	US-08-442-144A-81	Sequence 81, Appl
414	3	30.0	29	1	US-08-412-110-342	Sequence 342, App	C 487	3	30.0	33	3	US-08-442-144A-100	Sequence 100, App
415	3	30.0	29	1	US-08-412-110-342	Sequence 342, App	C 488	3	30.0	33	3	US-08-442-144A-100	Sequence 100, App
416	3	30.0	29	1	US-08-409-442A-342	Sequence 342, App	C 489	3	30.0	33	3	US-08-442-144A-103	Sequence 103, App
417	3	30.0	29	1	US-08-409-442A-342	Sequence 342, App	C 490	3	30.0	33	3	US-08-442-144A-103	Sequence 103, App
418	3	30.0	29	2	US-08-469-609A-342	Sequence 342, App	C 491	3	30.0	33	3	US-08-442-144A-113	Sequence 113, App
419	3	30.0	29	2	US-08-469-609A-342	Sequence 342, App	C 492	3	30.0	33	3	US-08-442-144A-113	Sequence 113, App
420	3	30.0	29	3	US-09-143-190-342	Sequence 342, App	C 493	3	30.0	33	3	US-08-935-268A-11	Sequence 11, Appl
421	3	30.0	29	3	US-09-143-190-342	Sequence 342, App	C 494	3	30.0	33	3	US-08-935-268A-11	Sequence 11, Appl
422	3	30.0	29	3	US-09-502-344-342	Sequence 342, App	C 495	3	30.0	33	3	US-08-441-970-81	Sequence 81, Appl
423	3	30.0	29	3	US-09-502-344-342	Sequence 342, App	C 496	3	30.0	33	3	US-08-441-970-81	Sequence 81, Appl
424	3	30.0	29	4	US-09-813-781-104	Sequence 104, App	C 497	3	30.0	33	3	US-08-441-970-81	Sequence 81, Appl
425	3	30.0	29	4	US-09-813-781-104	Sequence 104, App	C 498	3	30.0	33	3	US-08-441-970-100	Sequence 100, App
426	3	30.0	30	1	US-08-186-229-32	Sequence 32, Appl	C 499	3	30.0	33	3	US-08-441-970-100	Sequence 100, App
427	3	30.0	30	1	US-08-186-229-32	Sequence 32, Appl	C 500	3	30.0	33	3	US-08-441-970-103	Sequence 103, App
428	3	30.0	30	2	US-08-470-124-32	Sequence 32, Appl	C 501	3	30.0	33	3	US-08-441-970-103	Sequence 103, App
429	3	30.0	30	2	US-08-470-124-32	Sequence 32, Appl	C 502	3	30.0	33	3	US-08-441-970-113	Sequence 113, App
430	3	30.0	30	4	US-09-671-089-36	Sequence 36, Appl	C 503	3	30.0	33	3	US-08-441-970-113	Sequence 113, App
431	3	30.0	31	1	US-08-086-428B-112	Sequence 112, App	C 504	3	30.0	33	3	US-08-169-715-5	Sequence 5, Appl
432	3	30.0	31	1	US-08-086-428B-112	Sequence 112, App	C 505	3	30.0	33	3	US-08-169-715-5	Sequence 5, Appl
433	3	30.0	31	2	US-08-468-570-112	Sequence 112, App	C 506	3	30.0	33	3	US-08-169-715-19	Sequence 19, Appl
434	3	30.0	31	2	US-08-468-570-112	Sequence 112, App	C 507	3	30.0	33	3	US-08-169-715-19	Sequence 19, Appl
435	3	30.0	31	2	US-08-290-665A-216	Sequence 216, App	C 508	3	30.0	33	3	US-08-169-715-59	Sequence 59, Appl
436	3	30.0	31	2	US-08-290-665A-216	Sequence 216, App	C 509	3	30.0	33	3	US-08-169-715-59	Sequence 59, Appl
437	3	30.0	31	2	US-08-290-665A-216	Sequence 216, App	C 510	3	30.0	33	3	US-08-452-223-11	Sequence 11, Appl
438	3	30.0	31	4	US-08-466-601A-112	Sequence 112, App	C 511	3	30.0	33	3	US-08-452-223-11	Sequence 11, Appl
439	3	30.0	31	4	US-08-466-601A-112	Sequence 112, App	C 512	3	30.0	33	3	US-09-671-089-35	Sequence 35, Appl
440	3	30.0	31	5	PCT-US95-10398-216	Sequence 216, App	C 513	3	30.0	34	3	US-09-671-089-35	Sequence 35, Appl
441	3	30.0	33	1	US-08-138-608-7	Sequence 7, Appl	C 514	3	30.0	34	3	US-08-814-412-24	Sequence 24, Appl
442	3	30.0	33	1	US-08-138-608-7	Sequence 7, Appl	C 515	3	30.0	34	3	US-08-814-412-24	Sequence 24, Appl
443	3	30.0	33	1	US-08-138-608-11	Sequence 11, Appl	C 516	3	30.0	34	3	US-09-232-477-13	Sequence 13, Appl
444	3	30.0	33	1	US-08-138-608-11	Sequence 11, Appl	C 517	3	30.0	34	3	US-09-232-477-13	Sequence 13, Appl
445	3	30.0	33	1	US-08-438-639-6	Sequence 6, Appl	C 518	3	30.0	34	3	US-09-784-982-13	Sequence 13, Appl
446	3	30.0	33	1	US-08-438-639-6	Sequence 6, Appl	C 519	3	30.0	34	3	US-09-784-982-13	Sequence 13, Appl
447	3	30.0	33	1	US-08-438-639-6	Sequence 6, Appl	C 520	3	30.0	35	3	US-09-363-189B-9	Sequence 9, Appl
448	3	30.0	33	1	US-08-438-639-25	Sequence 25, Appl	C 521	3	30.0	35	3	US-09-363-189B-9	Sequence 9, Appl
449	3	30.0	33	1	US-08-438-639-28	Sequence 28, Appl	C 522	3	30.0	36	1	US-08-482-882-40	Sequence 40, Appl
450	3	30.0	33	1	US-08-438-639-28	Sequence 28, Appl	C 523	3	30.0	36	1	US-08-482-882-40	Sequence 40, Appl
451	3	30.0	33	1	US-08-438-639-38	Sequence 38, Appl	C 524	3	30.0	36	1	US-08-483-389-40	Sequence 40, Appl
452	3	30.0	33	1	US-08-438-639-38	Sequence 38, Appl	C 525	3	30.0	36	1	US-08-483-389-40	Sequence 40, Appl
453	3	30.0	33	1	US-07-813-338A-6	Sequence 6, Appl	C 526	3	30.0	36	2	US-08-487-113D-40	Sequence 40, Appl
454	3	30.0	33	1	US-07-813-338A-6	Sequence 6, Appl	C 527	3	30.0	36	2	US-08-487-113D-40	Sequence 40, Appl
455	3	30.0	33	1	US-07-813-338A-25	Sequence 25, Appl	C 528	3	30.0	36	2	US-08-726-528A-2	Sequence 2, Appl
456	3	30.0	33	1	US-07-813-338A-25	Sequence 25, Appl	C 529	3	30.0	36	2	US-08-726-528A-2	Sequence 2, Appl
457	3	30.0	33	1	US-07-813-338A-28	Sequence 28, Appl	C 530	3	30.0	36	2	US-08-785-571-3	Sequence 3, Appl
458	3	30.0	33	1	US-07-813-338A-28	Sequence 28, Appl	C 531	3	30.0	36	2	US-08-785-571-3	Sequence 3, Appl
459	3	30.0	33	1	US-07-813-338A-38	Sequence 38, Appl	C 532	3	30.0	36	2	US-08-473-503-40	Sequence 40, Appl
460	3	30.0	33	1	US-07-813-338A-38	Sequence 38, Appl	C 533	3	30.0	36	2	US-08-473-503-40	Sequence 40, Appl
461	3	30.0	33	2	US-08-452-242-11	Sequence 11, Appl	C 534	3	30.0	36	2	US-08-483-932-40	Sequence 40, Appl
462	3	30.0	33	2	US-08-452-242-11	Sequence 11, Appl	C 535	3	30.0	36	2	US-08-483-932-40	Sequence 40, Appl
463	3	30.0	33	3	US-08-453-176A-11	Sequence 11, Appl	C 536	3	30.0	36	2	US-08-720-420A-40	Sequence 40, Appl
464	3	30.0	33	3	US-08-453-176A-11	Sequence 11, Appl	C 537	3	30.0	36	2	US-08-720-420A-40	Sequence 40, Appl
465	3	30.0	33	3	US-08-441-971-81	Sequence 81, Appl	C 538	3	30.0	36	3	US-08-714-017-40	Sequence 40, Appl

539	3	30.0	3	US-08-475-680-40	Sequence 40, Appl	c 612	3	30.0	61	3	US-08-952-793-377	Sequence 377, App
540	3	30.0	36	US-08-475-680-40	Sequence 40, Appl	613	3	30.0	61	4	US-09-849-928-377	Sequence 377, App
541	3	30.0	36	PCT-US93-06734-3	Sequence 3, Appl	c 614	3	30.0	61	4	US-09-849-928-377	Sequence 377, App
542	3	30.0	36	PCT-US93-06734-3	Sequence 3, Appl	615	3	30.0	61	4	US-09-621-976-14754	Sequence 14754, A
543	3	30.0	36	PCT-US94-14106-26	Sequence 26, Appl	c 616	3	30.0	61	4	US-09-621-976-14754	Sequence 14754, A
544	3	30.0	36	PCT-US94-14106-26	Sequence 26, Appl	617	3	30.0	61	5	PCT-US96-09455A-377	Sequence 377, App
545	3	30.0	37	US-08-388-672A-5	Sequence 5, Appl	c 618	3	30.0	63	4	PCT-US96-09455A-377	Sequence 377, App
546	3	30.0	37	US-08-388-672A-5	Sequence 5, Appl	619	3	30.0	63	4	US-09-069-827A-17	Sequence 17, Appl
547	3	30.0	37	US-09-080-554-5	Sequence 5, Appl	c 620	3	30.0	64	4	US-09-069-827A-17	Sequence 17, Appl
548	3	30.0	37	US-09-080-554-5	Sequence 5, Appl	621	3	30.0	64	4	US-09-513-999C-25672	Sequence 25672, A
549	3	30.0	38	US-08-814-412-32	Sequence 32, Appl	c 622	3	30.0	64	4	US-09-513-999C-25672	Sequence 25672, A
550	3	30.0	38	US-08-814-412-32	Sequence 32, Appl	623	3	30.0	68	4	US-09-513-999C-16627	Sequence 16627, A
551	3	30.0	38	US-09-617-594A-13	Sequence 13, Appl	c 624	3	30.0	68	4	US-09-513-999C-16627	Sequence 16627, A
552	3	30.0	38	US-09-617-594A-13	Sequence 13, Appl	625	3	30.0	69	3	US-09-269-911A-7	Sequence 7, Appl
553	3	30.0	39	US-08-485-359-5	Sequence 5, Appl	c 626	3	30.0	69	3	US-09-269-911A-7	Sequence 7, Appl
554	3	30.0	39	US-08-485-359-5	Sequence 5, Appl	627	3	30.0	69	3	US-09-269-911A-8	Sequence 8, Appl
555	3	30.0	39	US-08-569-594-5	Sequence 5, Appl	c 628	3	30.0	69	3	US-09-269-911A-8	Sequence 8, Appl
556	3	30.0	39	US-08-569-594-5	Sequence 5, Appl	629	3	30.0	70	3	US-08-952-793-369	Sequence 369, App
557	3	30.0	39	US-08-444-644-2	Sequence 2, Appl	c 630	3	30.0	70	3	US-08-952-793-369	Sequence 369, App
558	3	30.0	39	US-08-444-644-2	Sequence 2, Appl	631	3	30.0	70	4	US-09-849-928-369	Sequence 369, App
559	3	30.0	39	US-08-444-644-6	Sequence 6, Appl	c 632	3	30.0	70	4	US-09-849-928-369	Sequence 369, App
560	3	30.0	39	US-08-444-644-6	Sequence 6, Appl	633	3	30.0	70	5	PCT-US96-09455A-369	Sequence 369, App
561	3	30.0	39	US-08-232-246A-2	Sequence 2, Appl	c 634	3	30.0	70	5	PCT-US96-09455A-369	Sequence 369, App
562	3	30.0	39	US-08-232-246A-2	Sequence 2, Appl	635	3	30.0	71	3	US-08-952-793-382	Sequence 382, App
563	3	30.0	39	US-08-232-246A-6	Sequence 6, Appl	c 636	3	30.0	71	3	US-08-952-793-382	Sequence 382, App
564	3	30.0	39	US-08-232-246A-6	Sequence 6, Appl	637	3	30.0	71	4	US-09-849-928-382	Sequence 382, App
565	3	30.0	39	US-09-564-329A-26	Sequence 26, Appl	c 638	3	30.0	71	4	US-09-849-928-382	Sequence 382, App
566	3	30.0	39	US-09-564-329A-26	Sequence 26, Appl	639	3	30.0	71	4	US-09-513-999C-27432	Sequence 27432, A
567	3	30.0	39	US-09-963-620-26	Sequence 26, Appl	c 640	3	30.0	71	4	US-09-513-999C-27432	Sequence 27432, A
568	3	30.0	39	US-09-963-620-26	Sequence 26, Appl	641	3	30.0	71	5	PCT-US96-09455A-382	Sequence 382, App
569	3	30.0	39	US-09-855-632-26	Sequence 26, Appl	c 642	3	30.0	71	5	PCT-US96-09455A-382	Sequence 382, App
570	3	30.0	39	US-09-855-632-26	Sequence 26, Appl	643	3	30.0	73	4	US-09-513-999C-19180	Sequence 19180, A
571	3	30.0	39	PCT-US96-08815-5	Sequence 5, Appl	c 644	3	30.0	73	4	US-09-513-999C-19180	Sequence 19180, A
572	3	30.0	39	PCT-US96-08815-5	Sequence 5, Appl	645	3	30.0	73	4	US-09-513-999C-25699	Sequence 25699, A
573	3	30.0	42	US-08-933-983-23	Sequence 23, Appl	c 646	3	30.0	73	4	US-09-513-999C-25699	Sequence 25699, A
574	3	30.0	42	US-08-933-983-23	Sequence 23, Appl	647	3	30.0	81	4	US-09-603-663-34	Sequence 34, Appl
575	3	30.0	42	US-09-502-653-25	Sequence 25, Appl	c 648	3	30.0	81	4	US-09-603-663-34	Sequence 34, Appl
576	3	30.0	42	US-09-502-653-25	Sequence 25, Appl	649	3	30.0	81	4	US-09-603-658-34	Sequence 34, Appl
577	3	30.0	45	US-08-987-943-6	Sequence 6, Appl	c 650	3	30.0	81	4	US-09-603-658-34	Sequence 34, Appl
578	3	30.0	45	US-08-987-943-6	Sequence 6, Appl	651	3	30.0	81	4	US-09-602-373A-34	Sequence 34, Appl
579	3	30.0	45	US-08-987-943-7	Sequence 7, Appl	c 652	3	30.0	81	4	US-09-602-373A-34	Sequence 34, Appl
580	3	30.0	45	US-08-987-943-7	Sequence 7, Appl	653	3	30.0	81	4	US-09-703-399A-36	Sequence 36, Appl
581	3	30.0	45	US-08-987-943-11	Sequence 11, Appl	c 654	3	30.0	81	4	US-09-703-399A-36	Sequence 36, Appl
582	3	30.0	45	US-08-987-943-11	Sequence 11, Appl	655	3	30.0	84	4	US-09-603-663-61	Sequence 61, Appl
583	3	30.0	47	US-09-422-978-3789	Sequence 3789, Ap	c 656	3	30.0	84	4	US-09-603-663-61	Sequence 61, Appl
584	3	30.0	47	US-09-422-978-3789	Sequence 3789, Ap	657	3	30.0	84	4	US-09-603-658-61	Sequence 61, Appl
585	3	30.0	48	US-08-230-002-8	Sequence 8, Appl	c 658	3	30.0	84	4	US-09-603-658-61	Sequence 61, Appl
586	3	30.0	48	US-08-230-002-8	Sequence 8, Appl	659	3	30.0	84	4	US-09-602-373A-61	Sequence 61, Appl
587	3	30.0	48	US-08-678-854-8	Sequence 8, Appl	c 660	3	30.0	84	4	US-09-602-373A-61	Sequence 61, Appl
588	3	30.0	48	US-08-678-854-8	Sequence 8, Appl	661	3	30.0	84	4	US-09-703-399A-58	Sequence 58, Appl
589	3	30.0	48	US-09-300-008B-63	Sequence 63, Appl	c 662	3	30.0	84	4	US-09-703-399A-58	Sequence 58, Appl
590	3	30.0	48	US-09-300-008B-63	Sequence 63, Appl	663	3	30.0	84	4	US-09-513-999C-25247	Sequence 25247, A
591	3	30.0	50	US-09-508-930D-32	Sequence 32, Appl	c 664	3	30.0	84	4	US-09-513-999C-25247	Sequence 25247, A
592	3	30.0	50	US-09-508-930D-32	Sequence 32, Appl	665	3	30.0	85	4	US-09-621-976-13884	Sequence 13884, A
593	3	30.0	51	US-09-546-934-30	Sequence 30, Appl	c 666	3	30.0	85	4	US-09-621-976-13884	Sequence 13884, A
594	3	30.0	51	US-09-546-934-30	Sequence 30, Appl	667	3	30.0	87	4	US-09-513-999C-18169	Sequence 18169, A
595	3	30.0	51	US-09-513-999C-27635	Sequence 27635, A	c 668	3	30.0	87	4	US-09-513-999C-18169	Sequence 18169, A
596	3	30.0	51	US-09-513-999C-27635	Sequence 27635, A	669	3	30.0	91	4	US-09-328-750A-5	Sequence 5, Appl
597	3	30.0	58	US-09-621-976-8641	Sequence 8641, Ap	c 670	3	30.0	91	4	US-09-328-750A-5	Sequence 5, Appl
598	3	30.0	58	US-09-621-976-8641	Sequence 8641, Ap	671	3	30.0	92	2	US-08-353-372A-16	Sequence 16, Appl
599	3	30.0	58	US-09-513-999C-30029	Sequence 30029, A	c 672	3	30.0	92	2	US-08-353-372A-16	Sequence 16, Appl
600	3	30.0	58	US-09-513-999C-30029	Sequence 30029, A	673	3	30.0	92	4	US-09-513-999C-18840	Sequence 18840, A
601	3	30.0	59	US-08-327-525A-14	Sequence 14, Appl	c 674	3	30.0	92	4	US-09-513-999C-18840	Sequence 18840, A
602	3	30.0	59	US-08-327-525A-14	Sequence 14, Appl	675	3	30.0	96	3	US-09-240-078-28	Sequence 28, Appl
603	3	30.0	59	US-08-531-137B-14	Sequence 14, Appl	c 676	3	30.0	96	3	US-09-240-078-28	Sequence 28, Appl
604	3	30.0	59	US-08-531-137B-14	Sequence 14, Appl	677	3	30.0	96	3	US-09-240-078-29	Sequence 29, Appl
605	3	30.0	59	US-09-158-765-14	Sequence 14, Appl	c 678	3	30.0	96	3	US-09-240-078-29	Sequence 29, Appl
606	3	30.0	59	US-09-158-765-14	Sequence 14, Appl	679	3	30.0	96	3	US-09-240-078-31	Sequence 31, Appl
607	3	30.0	59	US-09-796-071-14	Sequence 14, Appl	c 680	3	30.0	96	3	US-09-240-078-31	Sequence 31, Appl
608	3	30.0	59	US-09-796-071-14	Sequence 14, Appl	681	3	30.0	97	3	US-08-952-793-272	Sequence 272, App
609	3	30.0	59	US-09-049-805-14	Sequence 14, Appl	c 682	3	30.0	97	3	US-08-952-793-272	Sequence 272, App
610	3	30.0	59	US-09-049-805-14	Sequence 14, Appl	683	3	30.0	97	4	US-09-849-928-272	Sequence 272, App
611	3	30.0	61	US-08-952-793-377	Sequence 377, App	c 684	3	30.0	97	4	US-09-849-928-272	Sequence 272, App

685	3	30.0	97	4	US-09-513-999C-30390	Sequence 30390, A	c 758	2	20.0	7	3	US-09-134-246-2	Sequence 2, Appl
c 686	3	30.0	97	4	US-09-513-999C-30390	Sequence 30390, A	759	2	20.0	7	3	US-09-286-098-102	Sequence 102, App
687	3	30.0	97	5	PCT-US96-09455A-272	Sequence 272, App	c 760	2	20.0	7	3	US-09-286-098-102	Sequence 102, App
c 688	3	30.0	97	5	PCT-US96-09455A-272	Sequence 272, App	761	2	20.0	7	4	US-09-325-193A-88	Sequence 88, Appl
689	3	30.0	98	4	US-09-513-999C-20023	Sequence 20023, A	c 762	2	20.0	7	4	US-09-325-193A-88	Sequence 88, Appl
c 690	3	30.0	98	4	US-09-513-999C-20023	Sequence 20023, A	763	2	20.0	7	4	US-09-857-316-1	Sequence 1, Appl
691	3	30.0	98	4	US-09-513-999C-34152	Sequence 34152, A	c 764	2	20.0	7	4	US-09-857-316-1	Sequence 1, Appl
c 692	3	30.0	98	4	US-09-513-999C-34152	Sequence 34152, A	765	2	20.0	7	4	US-09-857-316-1	Sequence 1, Appl
693	3	30.0	100	4	US-09-513-999C-34152	Sequence 34152, A	c 766	2	20.0	7	4	US-09-641-540-21	Sequence 21, Appl
c 694	3	30.0	100	4	US-09-513-999C-29839	Sequence 29839, A	767	2	20.0	7	4	US-09-641-540-21	Sequence 21, Appl
695	2	20.0	4	1	US-08-368-071-5	Sequence 5, Appl	c 768	2	20.0	7	5	PCT-US94-05659-13	Sequence 13, Appl
c 696	2	20.0	4	1	US-08-368-071-5	Sequence 5, Appl	769	2	20.0	7	5	PCT-US94-05659-13	Sequence 13, Appl
697	2	20.0	4	1	US-08-458-181-5	Sequence 5, Appl	c 770	2	20.0	7	5	PCT-US95-04092-12	Sequence 12, Appl
c 698	2	20.0	4	1	US-08-458-181-5	Sequence 5, Appl	771	2	20.0	7	5	PCT-US95-04092-12	Sequence 12, Appl
699	2	20.0	4	1	US-08-458-181-5	Sequence 5, Appl	c 772	2	20.0	8	1	US-08-347-826A-13	Sequence 13, Appl
c 700	2	20.0	4	1	US-08-458-181-5	Sequence 5, Appl	773	2	20.0	8	1	US-08-347-826A-13	Sequence 13, Appl
701	2	20.0	4	1	PCT-US93-02172-5	Sequence 5, Appl	c 774	2	20.0	8	2	US-08-903-624-17	Sequence 17, Appl
c 702	2	20.0	4	1	PCT-US93-02172-5	Sequence 5, Appl	775	2	20.0	8	2	US-08-903-624-17	Sequence 17, Appl
703	2	20.0	5	1	US-07-630-288A-1	Sequence 1, Appl	c 776	2	20.0	8	3	US-08-646-301A-10	Sequence 10, Appl
c 704	2	20.0	5	1	US-07-630-288A-1	Sequence 1, Appl	777	2	20.0	8	3	US-08-646-301A-10	Sequence 10, Appl
705	2	20.0	5	1	US-07-630-288A-43	Sequence 43, Appl	c 778	2	20.0	8	3	US-09-030-701-3	Sequence 3, Appl
c 706	2	20.0	5	1	US-07-630-288A-43	Sequence 43, Appl	779	2	20.0	8	3	US-09-030-701-3	Sequence 3, Appl
707	2	20.0	5	1	US-08-468-049-1	Sequence 1, Appl	c 780	2	20.0	8	4	US-08-705-477B-106	Sequence 106, App
c 708	2	20.0	5	1	US-08-468-049-1	Sequence 1, Appl	781	2	20.0	8	4	US-08-705-477B-106	Sequence 106, App
709	2	20.0	5	1	US-08-468-049-43	Sequence 43, Appl	c 782	2	20.0	8	4	US-08-705-477B-108	Sequence 108, App
c 710	2	20.0	5	1	US-08-468-049-43	Sequence 43, Appl	783	2	20.0	8	4	US-08-705-477B-108	Sequence 108, App
711	2	20.0	5	4	US-09-933-313B-5	Sequence 5, Appl	c 784	2	20.0	8	4	US-09-601-537-21	Sequence 21, Appl
c 712	2	20.0	5	4	US-09-933-313B-5	Sequence 5, Appl	785	2	20.0	8	4	US-09-601-537-21	Sequence 21, Appl
713	2	20.0	5	4	US-10-037-927B-7	Sequence 7, Appl	c 786	2	20.0	8	4	US-09-915-060A-19	Sequence 19, Appl
c 714	2	20.0	5	4	US-10-037-927B-7	Sequence 7, Appl	787	2	20.0	8	4	US-09-915-060A-19	Sequence 19, Appl
715	2	20.0	5	4	US-09-975-413A-7	Sequence 7, Appl	c 788	2	20.0	9	1	US-08-566-037A-1	Sequence 1, Appl
c 716	2	20.0	5	4	US-09-975-413A-7	Sequence 7, Appl	789	2	20.0	9	1	US-08-566-037A-1	Sequence 1, Appl
717	2	20.0	5	4	US-09-957-005-6	Sequence 6, Appl	c 790	2	20.0	9	1	US-08-566-037A-6	Sequence 6, Appl
c 718	2	20.0	5	4	US-09-957-005-6	Sequence 6, Appl	791	2	20.0	9	1	US-08-566-037A-6	Sequence 6, Appl
719	2	20.0	5	4	US-09-510-238A-4	Sequence 4, Appl	c 792	2	20.0	9	1	US-08-153-848-20	Sequence 20, Appl
c 720	2	20.0	5	4	US-09-510-238A-4	Sequence 4, Appl	793	2	20.0	9	1	US-08-153-848-20	Sequence 20, Appl
721	2	20.0	5	4	US-09-966-997-8	Sequence 8, Appl	c 794	2	20.0	9	1	US-08-488-015B-20	Sequence 20, Appl
c 722	2	20.0	5	4	US-09-966-997-8	Sequence 8, Appl	795	2	20.0	9	1	US-08-488-015B-20	Sequence 20, Appl
723	2	20.0	6	1	US-08-169-950-4	Sequence 4, Appl	c 796	2	20.0	9	1	US-08-667-023-12	Sequence 12, Appl
c 724	2	20.0	6	1	US-08-169-950-4	Sequence 4, Appl	797	2	20.0	9	1	US-08-667-023-12	Sequence 12, Appl
725	2	20.0	6	1	US-08-133-179-7	Sequence 7, Appl	c 798	2	20.0	9	2	US-08-224-482-10	Sequence 10, Appl
c 726	2	20.0	6	1	US-08-133-179-7	Sequence 7, Appl	799	2	20.0	9	2	US-08-224-482-10	Sequence 10, Appl
727	2	20.0	6	2	US-08-692-825-19	Sequence 19, Appl	c 800	2	20.0	9	2	US-08-590-571-66	Sequence 66, Appl
c 728	2	20.0	6	2	US-08-692-825-19	Sequence 19, Appl	801	2	20.0	9	2	US-08-590-571-66	Sequence 66, Appl
729	2	20.0	6	2	US-08-468-819-25	Sequence 25, Appl	c 802	2	20.0	9	2	US-08-480-473B-26	Sequence 26, Appl
c 730	2	20.0	6	3	US-08-468-819-25	Sequence 25, Appl	803	2	20.0	9	2	US-08-480-473B-26	Sequence 26, Appl
731	2	20.0	6	3	US-09-037-135-2	Sequence 2, Appl	c 804	2	20.0	9	3	US-08-915-213-26	Sequence 26, Appl
c 732	2	20.0	6	3	US-09-037-135-2	Sequence 2, Appl	805	2	20.0	9	3	US-08-915-213-26	Sequence 26, Appl
733	2	20.0	6	3	US-08-895-495-19	Sequence 19, Appl	c 806	2	20.0	9	3	US-08-335-865J-12	Sequence 12, Appl
c 734	2	20.0	6	3	US-08-895-495-19	Sequence 19, Appl	807	2	20.0	9	3	US-08-335-865J-12	Sequence 12, Appl
735	2	20.0	6	3	US-09-404-670-1	Sequence 1, Appl	c 808	2	20.0	9	3	US-09-299-843A-20	Sequence 20, Appl
c 736	2	20.0	6	3	US-09-404-670-1	Sequence 1, Appl	809	2	20.0	9	3	US-09-299-843A-20	Sequence 20, Appl
737	2	20.0	6	3	US-09-404-671-1	Sequence 1, Appl	c 810	2	20.0	9	3	US-09-258-367-17	Sequence 17, Appl
c 738	2	20.0	6	3	US-09-404-671-1	Sequence 1, Appl	811	2	20.0	9	3	US-09-258-367-17	Sequence 17, Appl
739	2	20.0	6	3	US-08-646-301A-12	Sequence 12, Appl	c 812	2	20.0	9	3	US-09-258-367-17	Sequence 17, Appl
c 740	2	20.0	6	3	US-08-646-301A-12	Sequence 12, Appl	813	2	20.0	9	3	US-08-973-068-55	Sequence 55, Appl
741	2	20.0	6	3	US-09-030-701-1	Sequence 1, Appl	c 814	2	20.0	9	3	US-08-973-068-55	Sequence 55, Appl
c 742	2	20.0	6	3	US-09-030-701-1	Sequence 1, Appl	815	2	20.0	9	3	US-09-235-217-26	Sequence 26, Appl
743	2	20.0	6	3	US-09-286-098-101	Sequence 101, App	c 816	2	20.0	9	3	US-09-235-217-26	Sequence 26, Appl
c 744	2	20.0	6	3	US-09-286-098-101	Sequence 101, App	817	2	20.0	9	3	US-09-163-485-16	Sequence 16, Appl
745	2	20.0	6	3	US-09-401-869-1	Sequence 1, Appl	c 818	2	20.0	9	3	US-09-546-550-17	Sequence 17, Appl
c 746	2	20.0	6	3	US-09-401-869-1	Sequence 1, Appl	819	2	20.0	9	3	US-09-546-550-17	Sequence 17, Appl
747	2	20.0	6	3	US-09-401-870-1	Sequence 1, Appl	c 820	2	20.0	9	3	US-09-431-414-17	Sequence 17, Appl
c 748	2	20.0	6	3	US-09-401-870-1	Sequence 1, Appl	821	2	20.0	9	3	US-09-431-414-17	Sequence 17, Appl
749	2	20.0	6	3	US-09-404-056-1	Sequence 1, Appl	c 822	2	20.0	9	3	US-09-225-670-17	Sequence 17, Appl
c 750	2	20.0	6	3	US-09-404-056-1	Sequence 1, Appl	823	2	20.0	9	3	US-09-225-670-17	Sequence 17, Appl
751	2	20.0	6	4	US-09-325-193A-87	Sequence 87, Appl	c 824	2	20.0	9	3	US-09-008-097-9	Sequence 9, Appl
c 752	2	20.0	6	4	US-09-325-193A-87	Sequence 87, Appl	825	2	20.0	9	3	US-09-008-097-9	Sequence 9, Appl
753	2	20.0	6	4	US-09-632-538C-10	Sequence 10, Appl	c 826	2	20.0	9	3	US-08-623-428D-61	Sequence 61, Appl
c 754	2	20.0	6	4	US-09-632-538C-10	Sequence 10, Appl	827	2	20.0	9	3	US-08-623-428D-61	Sequence 61, Appl
755	2	20.0	6	4	US-09-213-383-25	Sequence 25, Appl	c 828	2	20.0	9	3	US-08-703-731A-4	Sequence 4, Appl
c 756	2	20.0	6	4	US-09-213-383-25	Sequence 25, Appl	829	2	20.0	9	3	US-08-703-731A-4	Sequence 4, Appl
757	2	20.0	7	2	US-08-853-703A-1	Sequence 1, Appl	c 830	2	20.0	9	3	US-08-431-349C-17	Sequence 17, Appl
c 758	2	20.0	7	2	US-08-853-703A-1	Sequence 1, Appl	831	2	20.0	9	3	US-08-431-349C-17	Sequence 17, Appl
759	2	20.0	7	3	US-09-134-246-2	Sequence 2, Appl	c 832	2	20.0	9	3	US-09-134-246-2	Sequence 2, Appl

831	2	20.0	9	3	US-09-088-337B-20	Sequence 20, Appl	c 904	2	20.0	10	4	US-08-912-951-105	Sequence 105, Appl
c 832	2	20.0	9	3	US-09-088-337B-20	Sequence 20, Appl	905	2	20.0	10	4	US-09-087-031E-8	Sequence 8, Appl
833	2	20.0	9	4	US-09-305-839-45	Sequence 45, Appl	c 906	2	20.0	10	4	US-09-087-031E-8	Sequence 8, Appl
c 834	2	20.0	9	4	US-09-305-839-45	Sequence 45, Appl	907	2	20.0	10	4	US-08-600-203-6	Sequence 6, Appl
835	2	20.0	9	4	US-09-803-263-13	Sequence 13, Appl	c 908	2	20.0	10	4	US-08-600-203-6	Sequence 6, Appl
c 836	2	20.0	9	4	US-09-803-263-13	Sequence 13, Appl	909	2	20.0	10	4	US-09-849-928-183	Sequence 183, Appl
837	2	20.0	9	4	US-09-472-667-9	Sequence 9, Appl	c 910	2	20.0	10	4	US-09-849-928-183	Sequence 183, Appl
c 838	2	20.0	9	4	US-09-472-667-9	Sequence 9, Appl	911	2	20.0	10	4	US-08-705-477E-107	Sequence 107, Appl
839	2	20.0	9	5	PCT-US93-11153-20	Sequence 20, Appl	c 912	2	20.0	10	4	US-08-705-477E-107	Sequence 107, Appl
c 840	2	20.0	9	5	PCT-US93-11153-20	Sequence 20, Appl	913	2	20.0	10	4	US-09-548-880B-2	Sequence 2, Appl
841	2	20.0	9	5	PCT-US96-10251-26	Sequence 26, Appl	c 914	2	20.0	10	4	US-09-548-880B-2	Sequence 2, Appl
c 842	2	20.0	9	5	PCT-US96-10251-26	Sequence 26, Appl	915	2	20.0	10	4	US-09-402-181B-105	Sequence 105, Appl
843	2	20.0	10	1	US-08-235-503B-3	Sequence 3, Appl	c 916	2	20.0	10	4	US-09-402-181B-105	Sequence 105, Appl
c 844	2	20.0	10	1	US-08-235-503B-3	Sequence 3, Appl	917	2	20.0	10	4	US-09-721-456-105	Sequence 105, Appl
845	2	20.0	10	1	US-08-351-748-12	Sequence 12, Appl	c 918	2	20.0	10	4	US-09-721-456-105	Sequence 105, Appl
c 846	2	20.0	10	1	US-08-351-748-12	Sequence 12, Appl	919	2	20.0	10	4	US-08-961-888-5	Sequence 5, Appl
847	2	20.0	10	1	US-08-430-536A-12	Sequence 12, Appl	c 920	2	20.0	10	4	US-08-961-888-5	Sequence 5, Appl
c 848	2	20.0	10	1	US-08-430-536A-12	Sequence 12, Appl	921	2	20.0	10	4	US-08-260-190-20	Sequence 20, Appl
849	2	20.0	10	1	US-08-122-433-14	Sequence 14, Appl	c 922	2	20.0	10	4	US-08-260-190-20	Sequence 20, Appl
c 850	2	20.0	10	1	US-08-122-433-14	Sequence 14, Appl	923	2	20.0	10	5	PCT-US93-02246-12	Sequence 12, Appl
851	2	20.0	10	1	US-08-250-740-36	Sequence 36, Appl	c 924	2	20.0	10	5	PCT-US93-02246-12	Sequence 12, Appl
c 852	2	20.0	10	1	US-08-250-740-36	Sequence 36, Appl	925	2	20.0	10	5	PCT-US93-08386-21	Sequence 21, Appl
853	2	20.0	10	1	US-08-472-255A-170	Sequence 170, Appl	c 926	2	20.0	10	5	PCT-US93-08386-21	Sequence 21, Appl
c 854	2	20.0	10	1	US-08-472-255A-170	Sequence 170, Appl	927	2	20.0	10	5	PCT-US94-04361-2	Sequence 2, Appl
855	2	20.0	10	1	US-08-479-724A-170	Sequence 170, Appl	c 928	2	20.0	10	5	PCT-US94-04361-2	Sequence 2, Appl
c 856	2	20.0	10	1	US-08-479-724A-170	Sequence 170, Appl	929	2	20.0	10	5	PCT-US95-05265-3	Sequence 3, Appl
857	2	20.0	10	1	US-08-591-989-58	Sequence 58, Appl	c 930	2	20.0	10	5	PCT-US95-05265-3	Sequence 3, Appl
c 858	2	20.0	10	1	US-08-591-989-58	Sequence 58, Appl	931	2	20.0	10	5	PCT-US95-05853-12	Sequence 12, Appl
859	2	20.0	10	1	US-08-414-398-1	Sequence 1, Appl	c 932	2	20.0	10	5	PCT-US95-05853-12	Sequence 12, Appl
c 860	2	20.0	10	1	US-08-414-398-1	Sequence 1, Appl	933	2	20.0	10	5	PCT-US95-05853-13	Sequence 13, Appl
861	2	20.0	10	2	US-08-590-571-14	Sequence 14, Appl	c 934	2	20.0	10	5	PCT-US95-05853-13	Sequence 13, Appl
c 862	2	20.0	10	2	US-08-590-571-14	Sequence 14, Appl	935	2	20.0	10	5	PCT-US95-05853-14	Sequence 14, Appl
863	2	20.0	10	2	US-08-627-151A-19	Sequence 19, Appl	c 936	2	20.0	10	5	PCT-US95-05853-14	Sequence 14, Appl
c 864	2	20.0	10	2	US-08-627-151A-19	Sequence 19, Appl	937	2	20.0	10	5	PCT-US95-05853-14	Sequence 14, Appl
865	2	20.0	10	2	US-08-676-279-30	Sequence 30, Appl	c 938	2	20.0	10	5	PCT-US96-04455A-183	Sequence 183, Appl
c 866	2	20.0	10	2	US-08-676-279-30	Sequence 30, Appl	939	2	20.0	10	5	PCT-US96-04455A-183	Sequence 183, Appl
867	2	20.0	10	2	US-08-480-473B-19	Sequence 19, Appl	c 940	2	20.0	10	5	PCT-US96-10251-19	Sequence 19, Appl
c 868	2	20.0	10	2	US-08-480-473B-19	Sequence 19, Appl	941	2	20.0	11	1	US-08-235-503B-21	Sequence 21, Appl
869	2	20.0	10	2	US-08-737-371A-12	Sequence 12, Appl	c 942	2	20.0	11	1	US-08-235-503B-21	Sequence 21, Appl
c 870	2	20.0	10	2	US-08-737-371A-12	Sequence 12, Appl	943	2	20.0	11	1	US-08-358-810A-6	Sequence 6, Appl
871	2	20.0	10	2	US-08-737-371A-13	Sequence 13, Appl	c 944	2	20.0	11	1	US-08-358-810A-6	Sequence 6, Appl
c 872	2	20.0	10	2	US-08-737-371A-13	Sequence 13, Appl	945	2	20.0	11	1	US-08-484-712A-6	Sequence 6, Appl
873	2	20.0	10	2	US-08-737-371A-14	Sequence 14, Appl	c 946	2	20.0	11	1	US-08-484-712A-6	Sequence 6, Appl
c 874	2	20.0	10	2	US-08-737-371A-14	Sequence 14, Appl	947	2	20.0	11	1	US-08-359-295C-2	Sequence 2, Appl
875	2	20.0	10	2	US-08-684-547-12	Sequence 12, Appl	c 948	2	20.0	11	1	US-08-359-295C-2	Sequence 2, Appl
c 876	2	20.0	10	2	US-08-684-547-12	Sequence 12, Appl	949	2	20.0	11	1	US-08-597-495B-21	Sequence 21, Appl
877	2	20.0	10	2	US-08-822-701-6	Sequence 6, Appl	c 950	2	20.0	11	1	US-08-597-495B-21	Sequence 21, Appl
c 878	2	20.0	10	2	US-08-822-701-6	Sequence 6, Appl	951	2	20.0	11	1	US-08-472-255A-121	Sequence 121, Appl
879	2	20.0	10	2	US-08-927-722-16	Sequence 16, Appl	c 952	2	20.0	11	1	US-08-472-255A-121	Sequence 121, Appl
c 880	2	20.0	10	2	US-08-927-722-16	Sequence 16, Appl	953	2	20.0	11	1	US-08-479-724A-121	Sequence 121, Appl
881	2	20.0	10	2	US-08-724-354D-13	Sequence 13, Appl	c 954	2	20.0	11	1	US-08-479-724A-121	Sequence 121, Appl
c 882	2	20.0	10	2	US-08-724-354D-13	Sequence 13, Appl	955	2	20.0	11	1	US-08-488-015B-14	Sequence 14, Appl
883	2	20.0	10	3	US-08-472-256B-170	Sequence 170, Appl	c 956	2	20.0	11	1	US-08-488-015B-14	Sequence 14, Appl
c 884	2	20.0	10	3	US-08-472-256B-170	Sequence 170, Appl	957	2	20.0	11	1	US-08-327-525A-34	Sequence 34, Appl
885	2	20.0	10	3	US-08-915-213-19	Sequence 19, Appl	c 958	2	20.0	11	1	US-08-327-525A-34	Sequence 34, Appl
c 886	2	20.0	10	3	US-08-915-213-19	Sequence 19, Appl	959	2	20.0	11	1	US-08-327-525A-35	Sequence 35, Appl
887	2	20.0	10	3	US-09-270-984A-13	Sequence 13, Appl	c 960	2	20.0	11	1	US-08-327-525A-35	Sequence 35, Appl
c 888	2	20.0	10	3	US-09-270-984A-13	Sequence 13, Appl	961	2	20.0	11	2	US-08-659-453B-3	Sequence 3, Appl
889	2	20.0	10	3	US-08-933-855-6	Sequence 6, Appl	c 962	2	20.0	11	2	US-08-659-453B-3	Sequence 3, Appl
c 890	2	20.0	10	3	US-08-933-855-6	Sequence 6, Appl	963	2	20.0	11	2	US-08-485-105A-2	Sequence 2, Appl
891	2	20.0	10	3	US-08-974-549A-105	Sequence 105, Appl	c 964	2	20.0	11	2	US-08-485-105A-2	Sequence 2, Appl
c 892	2	20.0	10	3	US-08-974-549A-105	Sequence 105, Appl	965	2	20.0	11	2	US-08-321-670-7	Sequence 7, Appl
893	2	20.0	10	3	US-09-235-217-19	Sequence 19, Appl	c 966	2	20.0	11	2	US-08-321-670-7	Sequence 7, Appl
c 894	2	20.0	10	3	US-09-235-217-19	Sequence 19, Appl	967	2	20.0	11	2	US-08-583-562B-18	Sequence 18, Appl
895	2	20.0	10	3	US-08-952-793-183	Sequence 183, Appl	c 968	2	20.0	11	2	US-08-583-562B-18	Sequence 18, Appl
c 896	2	20.0	10	3	US-08-952-793-183	Sequence 183, Appl	969	2	20.0	11	2	US-08-531-137B-34	Sequence 34, Appl
897	2	20.0	10	3	US-08-623-428D-56	Sequence 56, Appl	c 970	2	20.0	11	2	US-08-531-137B-34	Sequence 34, Appl
c 898	2	20.0	10	3	US-08-623-428D-56	Sequence 56, Appl	971	2	20.0	11	2	US-08-531-137B-35	Sequence 35, Appl
899	2	20.0	10	4	US-08-927-165A-39	Sequence 39, Appl	c 972	2	20.0	11	3	US-08-531-137B-35	Sequence 35, Appl
c 900	2	20.0	10	4	US-08-927-165A-39	Sequence 39, Appl	973	2	20.0	11	3	US-08-472-256B-121	Sequence 121, Appl
901	2	20.0	10	4	US-09-378-069A-16	Sequence 16, Appl	c 974	2	20.0	11	3	US-08-472-256B-121	Sequence 121, Appl
c 902	2	20.0	10	4	US-09-378-069A-16	Sequence 16, Appl	975	2	20.0	11	3	US-08-946-138-3	Sequence 3, Appl
903	2	20.0	10	4	US-08-912-951-105	Sequence 105, Appl	c 976	2	20.0	11	3	US-08-946-138-3	Sequence 3, Appl



977 2 20.0 11 3 US-08-862-431-6 Sequence 6, Appli  
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c 982 2 20.0 11 3 US-09-183-650-2 Sequence 2, Appli  
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987 2 20.0 11 3 US-08-675-816-13 Sequence 13, Appl  
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c 992 2 20.0 11 3 US-09-082-226A-3 Sequence 3, Appli  
993 2 20.0 11 3 US-09-269-911A-2 Sequence 2, Appli  
c 994 2 20.0 11 3 US-09-269-911A-2 Sequence 2, Appli  
995 2 20.0 11 3 US-09-130-862A-3 Sequence 3, Appli  
c 996 2 20.0 11 3 US-09-130-862A-3 Sequence 3, Appli  
997 2 20.0 11 3 US-09-158-765-34 Sequence 34, Appl  
c 998 2 20.0 11 3 US-09-158-765-34 Sequence 34, Appl  
999 2 20.0 11 3 US-09-158-765-34 Sequence 35, Appl  
c1000 2 20.0 11 3 US-09-158-765-35 Sequence 35, Appli

## ALIGNMENTS

RESULT 1  
US-08-330-535A-30  
; Sequence 30, Application US/08330535A  
; Patent No. 5659024  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Miyaehita, Toshiyuki  
; APPLICANT: Harigai, Masayoshi  
; APPLICANT: Hanada, Motoi  
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS  
; TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,535A  
; FILING DATE: 27-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/182,619  
; FILING DATE: 14-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 1174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-330-535A-30  
Query Match 100.0%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRRCWGYYY 10  
Db 10 RRRCWGYYY 1  
RESULT 3  
US-08-688-145-3  
; Sequence 3, Application US/08688145



; Patent No. 5744310  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: BAX Promoter Sequence and Screening  
; Patent No. 5744310  
; TITLE OF INVENTION: Assays for Identifying Agents that Regulate BAX Gene  
; TITLE OF INVENTION: Expression  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/688,145  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 1951  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-688-145-3  
Query Match 100.0%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RRCWGWYY 10  
Db 1 RRCWGWYY 10  
RESULT 4  
US-08-688-145-3/c  
; Sequence 3, Application US/08688145  
; Patent No. 5744310  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: BAX Promoter Sequence and Screening  
; Patent No. 5744310  
; TITLE OF INVENTION: Assays for Identifying Agents that Regulate BAX Gene  
; TITLE OF INVENTION: Expression  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/688,145  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 1951  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-688-145-3  
Query Match 100.0%; Score 10; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RRCWGWYY 10  
Db 10 RRCWGWYY 1  
RESULT 5  
US-08-838-844-30  
; Sequence 30, Application US/08838844  
; Patent No. 5908750  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Miyashita, Toshiyuki  
; APPLICANT: Harigai, Masayoshi  
; APPLICANT: Hanada, Motoi  
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS  
; TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL  
; TITLE OF INVENTION: DEATH  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,844  
; FILING DATE: 11-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/182,619  
; FILING DATE: 14-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,535  
; FILING DATE: 27-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 2520  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs

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/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-838-844-30

Query Match      100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10
Db 1 RRRCWGYYY 10

RESULT 6
US-08-838-844-30/c
; Sequence 30, Application US/08838844
; Patent No. 5908750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Miyashita, Toshiyuki
; APPLICANT: Harigai, Masayoshi
; APPLICANT: Hanada, Motoi
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS
; TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL
; TITLE OF INVENTION: DEATH
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,844
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/182,619
; FILING DATE: 14-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,535
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2520
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-838-844-30

Query Match      100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10
Db 10 RRRCWGYYY 1
```

```
RESULT 7
US-08-299-074A-3
; Sequence 3, Application US/08299074A
; Patent No. 595283
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
; TITLE OF INVENTION: BY P53
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,074A
; FILING DATE: 01-SEP-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,758
; FILING DATE: 31-MAR-1992
; APPLICATION NUMBER: 07/715,182
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-299-074A-3

Query Match      100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10
Db 1 RRRCWGYYY 10

RESULT 8
US-08-299-074A-3/c
; Sequence 3, Application US/08299074A
; Patent No. 5955263
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
; TITLE OF INVENTION: BY P53
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Witcoff
; STREET: 1001 G Street, NW
```

; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/299,074A  
; FILING DATE: 01-SEP-1994  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/860,758  
; FILING DATE: 31-MAR-1992  
; APPLICATION NUMBER: 07/715,182  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A  
; REGISTRATION NUMBER: 32141  
; REFERENCE/DOCKET NUMBER: 01107.47071  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-299-074A-3

Query Match 100.0%; Score 10; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYY 10  
||| |||||  
Db 10 RRRCWGYY 1

RESULT 9  
US-09-173-914-29/c  
; Sequence 29, Application US/09173914  
; Patent No. 6171857  
; GENERAL INFORMATION:  
; APPLICANT: Hendrickson, Eric  
; TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and  
; FILE REFERENCE: B0877/7017/HK  
; CURRENT APPLICATION NUMBER: US/09/173,914  
; CURRENT FILING DATE: 1998-10-16  
; EARLIER APPLICATION NUMBER: 60/064,557  
; EARLIER FILING DATE: 1997-10-17  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 29  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-173-914-29

Query Match 100.0%; Score 10; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYY 10  
||| |||||  
Db 1 RRRCWGYY 10

RESULT 10  
US-09-173-914-29/c  
; Sequence 29, Application US/09173914  
; Patent No. 6171857  
; GENERAL INFORMATION:  
; APPLICANT: Hendrickson, Eric  
; TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and  
; FILE REFERENCE: B0877/7017/HK  
; CURRENT APPLICATION NUMBER: US/09/173,914  
; CURRENT FILING DATE: 1998-10-16  
; EARLIER APPLICATION NUMBER: 60/064,557  
; EARLIER FILING DATE: 1997-10-17  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 29  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-173-914-29

Query Match 100.0%; Score 10; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYY 10  
||| |||||  
Db 10 RRRCWGYY 1

RESULT 11  
US-09-399-773-3  
; Sequence 3, Application US/09399773  
; Patent No. 6245515  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Sherman, Michael  
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING  
; TITLE OF INVENTION: BY P53  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff  
; STREET: 1001 G Street, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/399,773  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/299,074  
; FILING DATE:  
; APPLICATION NUMBER: 07/715,182  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A  
; REGISTRATION NUMBER: 32141  
; REFERENCE/DOCKET NUMBER: 01107.47071  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs

/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
US-09-399-773-3

Query Match 100.0%; Score 10; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10  
Db 1 RRRCWGYY 10

## RESULT 12

US-09-399-773-3/c  
/ Sequence 3, Application US/09399773  
/ Patent No. 6245515

## GENERAL INFORMATION:

/ APPLICANT: Vogelstein, Bert  
/ APPLICANT: Kinzler, Kenneth  
/ APPLICANT: Sherman, Michael  
/ TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING  
/ NUMBER OF SEQUENCES: 41

/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Banner & Witcoff  
/ STREET: 1001 G Street, NW  
/ CITY: Washington  
/ STATE: DC  
/ COUNTRY: USA  
/ ZIP: 20001

## COMPUTER READABLE FORM:

/ MEDIUM TYPE: Diskette  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: DOS  
/ SOFTWARE: FastSeq for Windows Version 2.0  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/399,773

## FILING DATE:

/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/299,074  
/ FILING DATE:  
/ APPLICATION NUMBER: 07/715,182  
/ FILING DATE: 14-JUN-1991  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Kagan, Sarah A  
/ REGISTRATION NUMBER: 32141  
/ REFERENCE/DOCKET NUMBER: 01107.47071  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-508-9100  
/ TELEFAX: 202-508-9299

## TELEX:

/ INFORMATION FOR SEQ ID NO: 3:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 10 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
US-09-399-773-3

Query Match 100.0%; Score 10; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10  
Db 10 RRRCWGYY 1

## RESULT 13

US-09-928-385B-24

/ Sequence 24, Application US/09928385B  
/ Patent No. 6544746  
/ GENERAL INFORMATION:

/ APPLICANT: Heyduk, Tomasz  
/ TITLE OF INVENTION: A Rapid and Sensitive Proximity-Based Assay for the Detection  
/ TITLE OF INVENTION: and Quantification of DNA Binding Proteins  
/ FILE REFERENCE: 16153-7963

/ CURRENT APPLICATION NUMBER: US/09/928,385B  
/ CURRENT FILING DATE: 2002-01-14  
/ NUMBER OF SEQ ID NOS: 24  
/ SEQ ID NO 24  
/ LENGTH: 10

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE:

/ NAME/KEY:

/ LOCATION:

/ OTHER INFORMATION: These sequences were chemically synthesized,

/ OTHER INFORMATION: but may also be created via recombinant methods.

US-09-928-385B-24

Query Match 100.0%; Score 10; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10

Db 1 RRRCWGYY 10

## RESULT 14

US-09-928-385B-24/c

/ Sequence 24, Application US/09928385B  
/ Patent No. 6544746  
/ GENERAL INFORMATION:

/ APPLICANT: Heyduk, Tomasz

/ TITLE OF INVENTION: A Rapid and Sensitive Proximity-Based Assay for the Detection  
/ TITLE OF INVENTION: and Quantification of DNA Binding Proteins  
/ FILE REFERENCE: 16153-7963

/ CURRENT APPLICATION NUMBER: US/09/928,385B  
/ CURRENT FILING DATE: 2002-01-14  
/ NUMBER OF SEQ ID NOS: 24  
/ SEQ ID NO 24  
/ LENGTH: 10

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE:

/ NAME/KEY:

/ LOCATION:

/ OTHER INFORMATION: These sequences were chemically synthesized,

/ OTHER INFORMATION: but may also be created via recombinant methods.

US-09-928-385B-24

Query Match 100.0%; Score 10; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10

Db 10 RRRCWGYY 1

## RESULT 15

US-08-260-190-21

/ Sequence 21, Application US/08260190A  
/ Patent No. 6774117

## GENERAL INFORMATION:

/ APPLICANT: Zavada, Jan

/ APPLICANT: Pastorekova, Silvia

/ APPLICANT: Pastorek, Jaromir

/ TITLE OF INVENTION: MN Gene and Protein

/ FILE REFERENCE: D-0021-2

/ CURRENT APPLICATION NUMBER: US/08/260,190A

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; CURRENT FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(10)
US-08-260-190-21
```

```
Query Match      100.0%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RRRCWGYYY 10
Db      1 RRRCWGYYY 10
|||||
```

```
RESULT 16
US-08-260-190-21/c
; Sequence 21, Application US/08260190A
; Patent No. 6774117
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaronir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/08/260,190A
; CURRENT FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(10)
US-08-260-190-21
```

```
Query Match      100.0%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RRRCWGYYY 10
Db      10 RRRCWGYYY 1
|||||
```

```
RESULT 17
US-09-210-748A-6
; Sequence 6, Application US/09210748A
; Patent No. 6335156
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
```

```
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; FILE REFERENCE: 1107.77810
; CURRENT APPLICATION NUMBER: US/09/210,748A
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/069,416
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-210-748A-6
```

```
Query Match      100.0%; Score 10; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RRRCWGYYY 10
Db      1 RRRCWGYYY 10
|||||
```

```
RESULT 18
US-09-210-748A-6/c
; Sequence 6, Application US/09210748A
; Patent No. 6335156
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; FILE REFERENCE: 1107.77810
; CURRENT APPLICATION NUMBER: US/09/210,748A
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/069,416
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-210-748A-6
```

```
Query Match      100.0%; Score 10; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RRRCWGYYY 10
Db      20 RRRCWGYYY 11
|||||
```

```
RESULT 19
US-09-939-581A-6
; Sequence 6, Application US/09939581A
; Patent No. 6740523
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; FILE REFERENCE: 1107.77810
; CURRENT APPLICATION NUMBER: US/09/939,581A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/210,748
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
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/ ORGANISM: Homo sapiens
US-09-939-581A-6
Query Match      100.0%; Score 10; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
Db 1 RRCWGWYYY 10

RESULT 20
US-09-939-581A-6/c
; Sequence 6, Application US/09939581A
; Patent No. 6740523
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; FILE REFERENCE: 1107.77810
; CURRENT APPLICATION NUMBER: US/09/939,581A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/210,748
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-939-581A-6
Query Match      100.0%; Score 10; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
Db 20 RRCWGWYYY 11

RESULT 21
US-08-713-052-4
; Sequence 4, Application US/08713052
; Patent No. 5840673
; GENERAL INFORMATION:
; APPLICANT: Buckbinder, Leonard R.
; APPLICANT: Kley, Nikolai
; TITLE OF INVENTION: Insulin-Like Growth Factor Binding
; TITLE OF INVENTION: Protein 3 (IGF-BP3) in Treatment of P53-Related Tumors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,052
; FILING DATE: 12-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaul, Timothy J.
; REGISTRATION NUMBER: 33,111
; REFERENCE/DOCKET NUMBER: DC38a
; TELEPHONE: (609) 252-5901
; TELEFAX: (609) 252-4526
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-713-052-4
Query Match      100.0%; Score 10; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
Db 21 RRCWGWYYY 12

RESULT 22
US-08-713-052-4/c
; Sequence 4, Application US/08713052
; Patent No. 5840673
; GENERAL INFORMATION:
; APPLICANT: Buckbinder, Leonard R.
; APPLICANT: Kley, Nikolai
; TITLE OF INVENTION: Insulin-Like Growth Factor Binding
; TITLE OF INVENTION: Protein 3 (IGF-BP3) in Treatment of P53-Related Tumors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,052
; FILING DATE: 12-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaul, Timothy J.
; REGISTRATION NUMBER: 33,111
; REFERENCE/DOCKET NUMBER: DC38a
; TELEPHONE: (609) 252-5901
; TELEFAX: (609) 252-4526
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-713-052-4
Query Match      100.0%; Score 10; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
Db 21 RRCWGWYYY 12
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```
RESULT 23
US-08-446-668-8
; Sequence 8, Application US/08446668
; Patent No. 6140058
; GENERAL INFORMATION:
; APPLICANT: Lane, David P.
; ADDRESS: Flehr Hobbach Test Albritton & Herbert LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,668
; FILING DATE: 24-JUL-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61269/WH/MTK
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-446-668-8

Query Match          90.0%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWGY 9
Db 1 RRCWGWGY 9

RESULT 24
US-08-446-668-8/c
; Sequence 8, Application US/08446668
; Patent No. 6140058
; GENERAL INFORMATION:
; APPLICANT: Lane, David P.
; ADDRESS: Flehr Hobbach Test Albritton & Herbert LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/446,668
; FILING DATE: 24-JUL-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61269/WH/MTK
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-446-668-8

Query Match          90.0%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCWGWYY 10
Db 9 RRCWGWYY 1

RESULT 25
US-09-196-099-15
; Sequence 15, Application US/09196099
; Patent No. 6465246
; GENERAL INFORMATION:
; APPLICANT: MUELLER, Rolf
; APPLICANT: SEDLACEK, Hans-Harald
; TITLE OF INVENTION: ONCOGENE- OR VIRUS-CONTROLLED EXPRESSION SYSTEM
; FILE REFERENCE: 26083/190
; CURRENT APPLICATION NUMBER: US/09/196,099
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: DE 19751587.8
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-196-099-15

Query Match          70.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWG 7
Db 1 RRCWGWG 7

RESULT 26
US-09-196-099-15/c
; Sequence 15, Application US/09196099
; Patent No. 6465246
; GENERAL INFORMATION:
; APPLICANT: MUELLER, Rolf
; APPLICANT: SEDLACEK, Hans-Harald
; TITLE OF INVENTION: ONCOGENE- OR VIRUS-CONTROLLED EXPRESSION SYSTEM
; FILE REFERENCE: 26083/190
; CURRENT APPLICATION NUMBER: US/09/196,099
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: DE 19751587.8
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
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/
/ ZIP: 20001
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/399,773
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/299,074
/ FILING DATE:
/ APPLICATION NUMBER: 07/715,182
/ FILING DATE: 14-JUN-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kagan, Sarah A
/ REGISTRATION NUMBER: 32141
/ REFERENCE/DOCKET NUMBER: 01107.47071
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-508-9100
/ TELEFAX: 202-508-9299
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 39:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-399-773-39
/
/ Query Match 50.0%; Score 5; DB 3; Length 5;
/ Best Local Similarity 100.0%; Pred. No. 0;
/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ Qy 1 RRCW 5
/ |||||
/ Db 1 RRCW 5
/
/ RESULT 30
/ US-09-399-773-39/c
/ Sequence 39, Application US/09399773
/ Patent No. 6245515
/ GENERAL INFORMATION:
/ APPLICANT: Vogelstein, Bert
/ APPLICANT: Kinzler, Kenneth
/ APPLICANT: Sherman, Michael
/ TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
/ TITLE OF INVENTION: BY P53
/ NUMBER OF SEQUENCES: 41
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Banner & Witcoff
/ STREET: 1001 G Street, NW
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20001
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/399,773
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/299,074
/ FILING DATE:
/ APPLICATION NUMBER: 07/715,182
/ FILING DATE: 14-JUN-1991
/ ATTORNEY/AGENT INFORMATION:
```

```
/
/
/ NAME: Kagan, Sarah A
/ REGISTRATION NUMBER: 32141
/ REFERENCE/DOCKET NUMBER: 01107.47071
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-508-9100
/ TELEFAX: 202-508-9299
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 39:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-399-773-39
/
/ Query Match 50.0%; Score 5; DB 3; Length 5;
/ Best Local Similarity 100.0%; Pred. No. 0;
/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ Qy 6 WGYYY 10
/ |||||
/ Db 5 WGYYY 1
/
/ RESULT 31
/ US-08-474-542A-134
/ Sequence 134, Application US/08474542A
/ Patent No. 5527898
/ GENERAL INFORMATION:
/ APPLICANT: Bauer, Heidi M.
/ APPLICANT: Gravitt, Patti E.
/ APPLICANT: Greer, Catherine E.
/ APPLICANT: Impraime, Chaka C.
/ APPLICANT: Manos, M. Michele
/ APPLICANT: Resnick, Robert M.
/ TITLE OF INVENTION: Detection of Human Papillomavirus by the
/ TITLE OF INVENTION: Polymerase Chain Reaction
/ NUMBER OF SEQUENCES: 298
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hoffmann-La Roche Inc.
/ STREET: 340 Kingsland Street
/ CITY: Nutley
/ STATE: New Jersey
/ COUNTRY: U.S.A.
/ ZIP: 07110
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/474,542A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Petry, Douglas A.
/ REGISTRATION NUMBER: 35,321
/ REFERENCE/DOCKET NUMBER: 9234
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (510) 814-2974
/ TELEFAX: (510) 814-2977
/ INFORMATION FOR SEQ ID NO: 134:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-474-542A-134
/
/ Query Match 50.0%; Score 5; DB 1; Length 20;
/ Best Local Similarity 100.0%; Pred. No. 0;
/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      5 WNGYY 9
Db      11 WNGYY 15

RESULT 32
US-08-474-542A-134/c
; Sequence 134, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Imprim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; METHOD OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,542A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 134:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-542A-134

Query Match      50.0%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RRCWW 6
Db      15 RRCWW 11

RESULT 33
US-08-457-648-134
; Sequence 134, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Imprim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; METHOD OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 134:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-457-648-134

Query Match      50.0%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WNGYY 9
Db      11 WNGYY 15

RESULT 34
US-08-457-648-134/c
; Sequence 134, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Imprim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; METHOD OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 134:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-457-648-134

Query Match      50.0%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WNGYY 9
Db      11 WNGYY 15
```

ATTORNEY/AGENT INFORMATION:  
NAME: Petry, Douglas A.  
REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 9205  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2974  
TELEFAX: (510) 814-2977  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-457-648-134

Query Match 50.0%; Score 5; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCWW 6  
Db 15 RRCWW 11

RESULT 35  
US-08-259-612A-9  
Sequence 9, Application US/08259612A  
Patent No. 5688918  
GENERAL INFORMATION:  
APPLICANT: Kulesz-Martin, Molly P.  
TITLE OF INVENTION: p53as PROTEIN AND ANTIBODY  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dunn & Associates, P.C.  
STREET: P.O. Box 96  
CITY: Newfane  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14108

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: Victor 300 SX/25 (IBM PC Compatible)  
OPERATING SYSTEM: MS-DOS Version 5.0  
SOFTWARE: Wordstar Professional Release 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/259,612A  
FILING DATE: 14-Jun-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/195,952  
FILING DATE: 14-Feb-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dunn, Michael L.  
REGISTRATION NUMBER: 25,330  
REFERENCE/DOCKET NUMBER: RPP:135B US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 433-1661  
TELEFAX: (716) 433-1665  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: Nucleic Acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Unknown  
MOLECULE TYPE:  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:

STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS: El - Diery et al.  
TITLE: DEFINITION OF A CONGENOUS BINDING  
TITLE: SITE FOR p53  
JOURNAL: Nature Genetics  
VOLUME: 1  
ISSUE:  
PAGES: 45-49  
DATE: April, 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-259-612A-9

Query Match 40.0%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWWG 7  
Db 4 CWWG 7

RESULT 36  
US-08-259-612A-9/c  
Sequence 9, Application US/08259612A  
Patent No. 5688918  
GENERAL INFORMATION:  
APPLICANT: Kulesz-Martin, Molly P.  
TITLE OF INVENTION: p53as PROTEIN AND ANTIBODY  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dunn & Associates, P.C.  
STREET: P.O. Box 96  
CITY: Newfane  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14108  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: Victor 300 SX/25 (IBM PC Compatible)  
OPERATING SYSTEM: MS-DOS Version 5.0  
SOFTWARE: Wordstar Professional Release 4  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/259,612A  
FILING DATE: 14-Jun-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/195,952  
FILING DATE: 14-Feb-1994



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;
;
; ISSUE:
; PAGES: 45-49
; DATE: April, 1992
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-644-291-9

Query Match 40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWG 7
Db 4 CWG 7

RESULT 38
US-08-644-291-9/c
; Sequence 9, Application US/08644291
; Patent No. 5726024
; GENERAL INFORMATION:
; APPLICANT: Kulesz-Martin, Molly P.
; TITLE OF INVENTION: p53as PROTEIN AND ANTIBODY
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dunn & Associates
; STREET: P.O. Box 96
; CITY: Newfane
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: Victor 300 SX/25 (IBM PC Compatible)
; OPERATING SYSTEM: MS-DOS Version 5.0
; SOFTWARE: Wordstar Professional Release 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,291
; FILING DATE: 10-May-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/259,612
; FILING DATE: 14-Jun-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/195,952
; FILING DATE: 11-Feb-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,496
; FILING DATE: 02-Aug-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Michael L.
; REGISTRATION NUMBER: 25,330
; REFERENCE/DOCKET NUMBER: RPP:135E US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 433-1661
; TELEFAX: (716) 433-1665
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: Nucleic Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE:
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE:
```

```
;
;
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: El - Diery et al.
; TITLE: DEFINITION OF A CONCENCUS BINDING
; TITLE: SITE FOR p53
; JOURNAL: Nature Genetics
; VOLUME: 1
; ISSUE:
; PAGES: 45-49
; DATE: April, 1992
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-644-291-9

Query Match 40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWG 7
Db 7 CWG 4

RESULT 39
US-09-672-717-212
; Sequence 212, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1,17,18
; OTHER INFORMATION: y=sum
; NAME/KEY: modified_base
; LOCATION: 19
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```

; OTHER INFORMATION: y=cm
; OTHER INFORMATION: based on Homo sapiens
US-09-672-717-212

Query Match 40.0%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10
DB 16 GYYY 19
|||||

RESULT 40
US-09-672-717-212/c
; Sequence 212, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1,17,18
; OTHER INFORMATION: y=um
; NAME/KEY: modified_base
; LOCATION: 19
; OTHER INFORMATION: y=cm
; OTHER INFORMATION: based on Homo sapiens
US-09-672-717-212

Query Match 40.0%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRR 4
DB 19 RRRR 16
|||||

RESULT 41
US-08-474-542A-133
; Sequence 133, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraime, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,542A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petty, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 133:

Query Match 40.0%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWGY 8
DB 11 WWGY 14
|||||

RESULT 42
US-08-474-542A-133/c
; Sequence 133, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraime, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,542A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petty, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 133:

```

SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-474-542A-133

Query Match 40.0%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 RCW 6  
Db 14 RCW 11

## RESULT 43

US-08-474-542A-135  
; Sequence 135, Application US/08474542A  
; Patent No. 5527898  
; GENERAL INFORMATION:  
; APPLICANT: Bauer, Heidi M.  
; APPLICANT: Gravitt, Patti E.  
; APPLICANT: Greer, Catherine E.  
; APPLICANT: Impraime, Chaka C.  
; APPLICANT: Manos, M. Michele  
; APPLICANT: Resnick, Robert M.  
; TITLE OF INVENTION: Detection of Human Papillomavirus by the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 298  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,542A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry, Douglas A.  
; REGISTRATION NUMBER: 35,321  
; REFERENCE/DOCKET NUMBER: 9234  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2974  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 135:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-474-542A-135

Query Match 40.0%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 WGY 9  
Db 12 WGY 15

## RESULT 44

US-08-474-542A-135/c  
; Sequence 135, Application US/08474542A  
; Patent No. 5527898  
; GENERAL INFORMATION:  
; APPLICANT: Bauer, Heidi M.  
; APPLICANT: Gravitt, Patti E.  
; APPLICANT: Greer, Catherine E.  
; APPLICANT: Impraime, Chaka C.  
; APPLICANT: Manos, M. Michele  
; APPLICANT: Resnick, Robert M.  
; TITLE OF INVENTION: Detection of Human Papillomavirus by the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 298  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,542A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry, Douglas A.  
; REGISTRATION NUMBER: 35,321  
; REFERENCE/DOCKET NUMBER: 9234  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2974  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 135:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-474-542A-135

Query Match 40.0%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCW 5  
Db 15 RRCW 12

## RESULT 45

US-08-457-648-133  
; Sequence 133, Application US/08457648  
; Patent No. 5639871  
; GENERAL INFORMATION:  
; APPLICANT: Bauer, Heidi M.  
; APPLICANT: Gravitt, Patti E.  
; APPLICANT: Greer, Catherine E.  
; APPLICANT: Impraime, Chaka C.  
; APPLICANT: Manos, M. Michele  
; APPLICANT: Resnick, Robert M.  
; TITLE OF INVENTION: Detection of Human Papillomavirus by the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 298  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey

COUNTRY: U.S.A.  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/457,648  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Petry, Douglas A.  
REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 9205  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2974  
TELEFAX: (510) 814-2977  
INFORMATION FOR SEQ ID NO: 133:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-457-648-133

Query Match 40.0%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WGGY 8  
DB 11 WGGY 14

RESULT 46  
US-08-457-648-133/c  
Sequence 133, Application US/08457648  
Patent No. 5639871  
GENERAL INFORMATION:  
APPLICANT: Bauer, Heidi M.  
APPLICANT: Gravitt, Patti E.  
APPLICANT: Greer, Catherine E.  
APPLICANT: Impra, Chaka C.  
APPLICANT: Manos, M. Michele  
APPLICANT: Resnick, Robert M.  
TITLE OF INVENTION: Detection of Human Papillomavirus by the  
NUMBER OF SEQUENCES: 298  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/457,648  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Petry, Douglas A.  
REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 9205  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2974  
TELEFAX: (510) 814-2977

INFORMATION FOR SEQ ID NO: 133:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-457-648-133

Query Match 40.0%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RCWW 6  
DB 14 RCWW 11

RESULT 47  
US-08-457-648-135  
Sequence 135, Application US/08457648  
Patent No. 5639871  
GENERAL INFORMATION:  
APPLICANT: Bauer, Heidi M.  
APPLICANT: Gravitt, Patti E.  
APPLICANT: Greer, Catherine E.  
APPLICANT: Impra, Chaka C.  
APPLICANT: Manos, M. Michele  
APPLICANT: Resnick, Robert M.  
TITLE OF INVENTION: Detection of Human Papillomavirus by the  
NUMBER OF SEQUENCES: 298  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/457,648  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Petry, Douglas A.  
REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 9205  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2974  
TELEFAX: (510) 814-2977  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-457-648-135

Query Match 40.0%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WGGY 9  
DB 12 WGGY 15



RESULT 48  
US-08-457-648-135/c  
; Sequence 135, Application US/08457648  
; Patent No. 5639871  
; GENERAL INFORMATION:  
; APPLICANT: Bauer, Heidi M.  
; APPLICANT: Gravitt, Patti E.  
; APPLICANT: Greer, Catherine E.  
; APPLICANT: Imprim, Chaka C.  
; APPLICANT: Manos, M. Michele  
; APPLICANT: Reenick, Robert M.  
; TITLE OF INVENTION: Detection of Human Papillomavirus by the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 298  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/457,648  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry, Douglas A.  
; REGISTRATION NUMBER: 35,321  
; REFERENCE/DOCKET NUMBER: 9205  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2974  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 135:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-457-648-135

Query Match 40.0%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCW 5  
Db 15 RRCW 12

RESULT 49  
US-08-657-828A-3  
; Sequence 3, Application US/08657828A  
; Patent No. 5876711  
; GENERAL INFORMATION:  
; APPLICANT: Fattaey, Ali  
; TITLE OF INVENTION: Methods and Compositions for Determining  
; TITLE OF INVENTION: the Tumor Suppressor Status of Cells  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Onyx Pharmaceuticals, Inc.  
; STREET: 3031 Research Drive  
; CITY: Richmond  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94806  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/657,828A  
; FILING DATE: 31-MAY-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Giotta, Gregory  
; REGISTRATION NUMBER: 32,028  
; REFERENCE/DOCKET NUMBER: ONYX1021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-8710  
; TELEFAX: 510-758-3405  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-657-828A-3

Query Match 40.0%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCR 4  
Db 1 RRCR 4

RESULT 50  
US-08-657-828A-3/c  
; Sequence 3, Application US/08657828A  
; Patent No. 5876711  
; GENERAL INFORMATION:  
; APPLICANT: Fattaey, Ali  
; TITLE OF INVENTION: Methods and Compositions for Determining  
; TITLE OF INVENTION: the Tumor Suppressor Status of Cells  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Onyx Pharmaceuticals, Inc.  
; STREET: 3031 Research Drive  
; CITY: Richmond  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94806  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/657,828A  
; FILING DATE: 31-MAY-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Giotta, Gregory  
; REGISTRATION NUMBER: 32,028  
; REFERENCE/DOCKET NUMBER: ONYX1021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-8710  
; TELEFAX: 510-758-3405  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

;  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-657-828A-3

Query Match 40.0%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRC 4  
|  
|  
|  
|  
Db 20 RRC 17

## RESULT 51

US-09-260-420-3  
; Sequence 3, Application US/09260420  
; Patent No. 6391630

; GENERAL INFORMATION:

; APPLICANT: Fattaey, Ali  
; TITLE OF INVENTION: Methods and Compositions for Determining  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Onyx Pharmaceuticals, Inc.  
; STREET: 3031 Research Drive  
; CITY: Richmond  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94806

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/260,420  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/657,828  
; FILING DATE: 31-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Giotta, Gregory  
; REGISTRATION NUMBER: 32,028  
; REFERENCE/DOCKET NUMBER: ONYX1021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-8710  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-260-420-3

Query Match 40.0%; Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRC 4  
|  
|  
|  
|  
Db 1 RRC 4

## RESULT 52

US-09-260-420-3/c

; Sequence 3, Application US/09260420  
; Patent No. 6391630

; GENERAL INFORMATION:

; APPLICANT: Fattaey, Ali  
; TITLE OF INVENTION: Methods and Compositions for Determining  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Onyx Pharmaceuticals, Inc.  
; STREET: 3031 Research Drive  
; CITY: Richmond  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94806

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/260,420  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/657,828  
; FILING DATE: 31-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Giotta, Gregory  
; REGISTRATION NUMBER: 32,028  
; REFERENCE/DOCKET NUMBER: ONYX1021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-262-8710  
; TELEFAX: 510-758-3405  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-260-420-3

Query Match 40.0%; Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRC 4  
|  
|  
|  
|  
Db 20 RRC 17

## RESULT 53

US-07-959-119A-8  
; Sequence 8, Application US/07959119A  
; Patent No. 5487985

; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John T.

; APPLICANT: Sorge, Joseph A.

; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 2730 Sand Hill Road  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94025

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/959,119A  
;; FILING DATE: 09-OCT-1992  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Halluin, Albert P.  
;; REGISTRATION NUMBER: 25,227  
;; REFERENCE/DOCKET NUMBER: 8142-021  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 854-3660  
;; TELEFAX: (415) 854-3694  
;; TELEX: 66141PENNIE  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 27 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-07-959-119A-8

Query Match 40.0%; Score 4; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCR 4  
Db 15 RRCR 18

RESULT 54  
US-07-959-119A-8/c  
; Sequence 8, Application US/07959119A  
; Patent No. 5487985  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John T.  
; APPLICANT: Sorge, Joseph A.  
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain  
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 2730 Sand Hill Road  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94025

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/959,119A  
FILING DATE: 09-OCT-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 8142-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 854-3660  
TELEFAX: (415) 854-3694  
TELEX: 66141PENNIE

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-959-119A-8

Query Match 40.0%; Score 4; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10  
Db 18 GYYY 15

RESULT 55  
US-07-959-119A-9  
; Sequence 9, Application US/07959119A  
; Patent No. 5487985  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John T.  
; APPLICANT: Sorge, Joseph A.  
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain  
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 2730 Sand Hill Road  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94025

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/959,119A  
FILING DATE: 09-OCT-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 8142-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 854-3660  
TELEFAX: (415) 854-3694  
TELEX: 66141PENNIE

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-959-119A-9

Query Match 40.0%; Score 4; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCR 4  
Db 15 RRCR 18

RESULT 56  
US-07-959-119A-9/c  
; Sequence 9, Application US/07959119A  
; Patent No. 5487985  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John T.  
; APPLICANT: Sorge, Joseph A.  
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain  
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes

16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 2730 Sand Hill Road  
CITY: Menlo Park  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/959,119A  
FILING DATE: 09-OCT-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 8142-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 854-3660  
TELEFAX: (415) 854-3694  
TELEX: 66141PENNIE  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-959-119A-9

Query Match 40.0%; Score 4; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10  
DB 18 GYYY 15

RESULT 57  
US-08-471-994-7  
Sequence 7, Application US/08471994  
Patent No. 5861245  
GENERAL INFORMATION:  
APPLICANT: McClelland, Michael  
APPLICANT: Welsh, John T.  
APPLICANT: Sorge, Joseph A.  
TITLE OF INVENTION: ARBITRARILY PRIMED POLYMERASE CHAIN  
TITLE OF INVENTION: REACTION METHOD FOR FINGERPRINTING GENOMES  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,994  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 8142-103  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-471-994-7

Query Match 40.0%; Score 4; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRR 4  
DB 15 RRRR 18

RESULT 58  
US-08-471-994-7/C  
Sequence 7, Application US/08471994  
Patent No. 5861245  
GENERAL INFORMATION:  
APPLICANT: McClelland, Michael  
APPLICANT: Welsh, John T.  
APPLICANT: Sorge, Joseph A.  
TITLE OF INVENTION: ARBITRARILY PRIMED POLYMERASE CHAIN  
TITLE OF INVENTION: REACTION METHOD FOR FINGERPRINTING GENOMES  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,994  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 8142-103  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-471-994-7

Query Match 40.0%; Score 4; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10  
DB 18 GYYY 15

Db 18 GYY 15

RESULT 59  
US-08-471-994-11  
; Sequence 11, Application US/08471994  
; Patent No. 5861245  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John T.  
; APPLICANT: Sorge, Joseph A.  
; TITLE OF INVENTION: ARBITRARILY PRIMED POLYMERASE CHAIN  
; TITLE OF INVENTION: REACTION METHOD FOR FINGERPRINTING GENOMES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,994  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8142-103  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-471-994-11

Query Match 40.0%; Score 4; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRC 4  
| | | |  
Db 15 RRC 18

RESULT 60  
US-08-471-994-11/c  
; Sequence 11, Application US/08471994  
; Patent No. 5861245  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John T.  
; APPLICANT: Sorge, Joseph A.  
; TITLE OF INVENTION: ARBITRARILY PRIMED POLYMERASE CHAIN  
; TITLE OF INVENTION: REACTION METHOD FOR FINGERPRINTING GENOMES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America

; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,994  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8142-103  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-08-471-994-11

Query Match 40.0%; Score 4; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYY 10  
| | | |  
Db 18 GYY 15

RESULT 61  
US-08-154-364-7  
; Sequence 7, Application US/08154364  
; Patent No. 6207810  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John T.  
; APPLICANT: Sorge, Joseph A.  
; TITLE OF INVENTION: ARBITRARILY PRIMED  
; TITLE OF INVENTION: POLYMERASE CHAIN  
; TITLE OF INVENTION: REACTION METHOD FOR FINGER PRINTING  
; TITLE OF INVENTION: GENOMES  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Limbach and Limbach  
; STREET: 2001 Ferry Building  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0,  
; SOFTWARE: Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/154,364  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bortner, Scott R.  
; REGISTRATION NUMBER: 34,298  
; REFERENCE/DOCKET NUMBER: STRG-20142 USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-433-4150  
; TELEFAX: 414-433-8716

; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-154-364-7

Query Match 40.0%; Score 4; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRC 4  
DB 15 RRC 18

RESULT 62  
US-08-154-364-7/c  
; Sequence 7, Application US/08154364  
; Patent No. 6207810  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John T.  
; TITLE OF INVENTION: ARBITRARILY PRIMED  
; TITLE OF INVENTION: POLYMERASE CHAIN  
; TITLE OF INVENTION: REACTION METHOD FOR FINGER PRINTING  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Limbach and Limbach  
; STREET: 2001 Ferry Building  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0,  
SOFTWARE: Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE:  
APPLICATION NUMBER: US/08/154,364

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Borthner, Scott R.  
REGISTRATION NUMBER: 34,298  
REFERENCE/DOCKET NUMBER: STRG-20142 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-433-4150  
TELEFAX: 414-433-8716

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-154-364-7

Query Match 40.0%; Score 4; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYY 10

Db 18 GYY 15

RESULT 63  
US-08-397-335-8  
; Sequence 8, Application US/08397335  
; Patent No. 6696277  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John T.  
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain  
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennle & Edmonds  
; STREET: 2730 Sand Hill Road  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,335  
FILING DATE: Concurrently herewith.  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/959,119  
FILING DATE: 09-DEC-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 8142-092  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 854-3660  
TELEFAX: (415) 854-3694  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-397-335-8

Query Match 40.0%; Score 4; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRC 4  
DB 15 RRC 18

RESULT 64  
US-08-397-335-8/c  
; Sequence 8, Application US/08397335  
; Patent No. 6696277  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John T.  
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain  
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennle & Edmonds

```

; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,335
; FILING DATE: Concurrently herewith.
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,119
; FILING DATE: 09-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-397-335-8

Query Match 40.0%; Score 4; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10
Db 18 GYYY 15

RESULT 65
US-08-397-335-9
; Sequence 9, Application US/08397335
; Patent No. 6696277
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,335
; FILING DATE: Concurrently herewith.
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,119
; FILING DATE: 09-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-397-335-9
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-397-335-9

Query Match 40.0%; Score 4; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4
Db 15 RRRC 18

RESULT 66
US-08-397-335-9/c
; Sequence 9, Application US/08397335
; Patent No. 6696277
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,335
; FILING DATE: Concurrently herewith.
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,119
; FILING DATE: 09-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-397-335-9
```

Query Match 40.0%; Score 4; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYY 10  
|||  
Db 18 GYY 15

RESULT 67  
US-09-347-343-1  
; Sequence 1, Application US/09347343A  
; Patent No. 6514948  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eyal R.  
; APPLICANT: KOBAYASHI, Hiroko  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE  
; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/09/347,343A  
; CURRENT FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-09-347-343-1

Query Match 30.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
|||  
Db 1 RRC 3

RESULT 68  
US-09-347-343-1/c  
; Sequence 1, Application US/09347343A  
; Patent No. 6514948  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eyal R.  
; APPLICANT: KOBAYASHI, Hiroko  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE  
; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/09/347,343A  
; CURRENT FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-09-347-343-1

Query Match 30.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
|||  
Db 6 RRC 4

RESULT 69  
US-09-347-343-2  
; Sequence 2, Application US/09347343A  
; Patent No. 6514948  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eyal R.  
; APPLICANT: KOBAYASHI, Hiroko  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE

; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/09/347,343A  
; CURRENT FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-09-347-343-2

Query Match 30.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYY 9  
|||  
Db 4 GYY 6

RESULT 70  
US-09-347-343-2/c  
; Sequence 2, Application US/09347343A  
; Patent No. 6514948  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eyal R.  
; APPLICANT: KOBAYASHI, Hiroko  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE  
; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/09/347,343A  
; CURRENT FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-09-347-343-2

Query Match 30.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
|||  
Db 6 RRC 4

RESULT 71  
US-09-936-552A-4  
; Sequence 4, Application US/09936552A  
; Patent No. 6610907  
; GENERAL INFORMATION:  
; APPLICANT: INSTITUTE OF GENETICS, CHINESE ACADEMY OF SCIENCES  
; APPLICANT: Zhu, Zhen  
; APPLICANT: Xie, Yinggu  
; APPLICANT: Liu, Yule  
; TITLE OF INVENTION: COTTON LEAF CURL VIRUS (CLCV) PROMOTER AND ITS USE  
; FILE REFERENCE: 2896-4001  
; CURRENT APPLICATION NUMBER: US/09/936,552A  
; CURRENT FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: CN 99103044.3  
; PRIOR FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Cotton leaf curl virus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(3)  
; OTHER INFORMATION: y=pyrimidine

US-09-936-552A-4  
; Sequence 4, Application US/09936552A  
; Patent No. 6610907  
; GENERAL INFORMATION:  
; APPLICANT: INSTITUTE OF GENETICS, CHINESE ACADEMY OF SCIENCES  
; APPLICANT: Zhu, Zhen  
; APPLICANT: Xie, Yinggu  
; APPLICANT: Liu, Yule  
; TITLE OF INVENTION: COTTON LEAF CURL VIRUS (CLCV) PROMOTER AND ITS USE  
; FILE REFERENCE: 2896-4001  
; CURRENT APPLICATION NUMBER: US/09/936,552A  
; CURRENT FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: CN 99103044.3  
; PRIOR FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Cotton leaf curl virus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(3)  
; OTHER INFORMATION: y=pyrimidine



; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5)\_(5)  
; OTHER INFORMATION: y-pyrimidine  
US-09-936-552A-4

Query Match 30.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
|||  
DB 1 YYY 3

RESULT 72  
US-09-936-552A-4/c  
; Sequence 4, Application US/09936552A  
; Patent No. 6610907  
; GENERAL INFORMATION:  
; APPLICANT: INSTITUTE OF GENETICS, CHINESE ACADEMY OF SCIENCES  
; APPLICANT: Zhu, Zhen  
; APPLICANT: Xie, Yingqiu  
; APPLICANT: Liu, Yule  
; TITLE OF INVENTION: COTTON LEAF CURL VIRUS (CLCUV) PROMOTER AND ITS USE  
; FILE REFERENCE: 2896-4001  
; CURRENT APPLICATION NUMBER: US/09/936,552A  
; CURRENT FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: CN 99103044.3  
; PRIOR FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Cotton leaf curl virus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)\_(3)  
; OTHER INFORMATION: y-pyrimidine  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5)\_(5)  
; OTHER INFORMATION: y-pyrimidine  
US-09-936-552A-4

Query Match 30.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
|||  
DB 3 RRR 1

RESULT 73  
US-09-263-692A-8  
; Sequence 8, Application US/09263692A  
; Patent No. 6639065  
; GENERAL INFORMATION:  
; APPLICANT: Council of Scientific and Industrial Research  
; TITLE OF INVENTION: A chemically synthesized artificial promoter for high level expression  
; FILE REFERENCE: Q52511  
; CURRENT APPLICATION NUMBER: US/09/263,692A  
; CURRENT FILING DATE: 1999-03-05  
; PRIOR APPLICATION NUMBER: 3322/Del/98  
; PRIOR FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: DNA

; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: domain II(b)  
US-09-263-692A-8

Query Match 30.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWW 6  
|||  
DB 1 CWW 3

RESULT 74  
US-09-263-692A-8/c  
; Sequence 8, Application US/09263692A  
; Patent No. 6639065  
; GENERAL INFORMATION:  
; APPLICANT: Council of Scientific and Industrial Research  
; TITLE OF INVENTION: A chemically synthesized artificial promoter for high level expression  
; FILE REFERENCE: Q52511  
; CURRENT APPLICATION NUMBER: US/09/263,692A  
; CURRENT FILING DATE: 1999-03-05  
; PRIOR APPLICATION NUMBER: 3322/Del/98  
; PRIOR FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: domain II(b)  
US-09-263-692A-8

Query Match 30.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WVG 7  
|||  
DB 6 WVG 4

RESULT 75  
US-08-646-301A-9  
; Sequence 9, Application US/08646301A  
; Patent No. 6194211  
; GENERAL INFORMATION:  
; APPLICANT: Richards, Cynthia Ann  
; APPLICANT: Huber, Brian E.  
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic Antigen for Expression Targeting  
; FILE REFERENCE: PB1508USW  
; CURRENT APPLICATION NUMBER: US/08/646,301A  
; CURRENT FILING DATE: 1996-05-16  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: consensus  
; OTHER INFORMATION: sequence B2 from DNA Sequence 1:3-11 (1990).  
; Patent No. 6194211  
US-08-646-301A-9

Query Match 30.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WNG 7  
|||  
Db 6 WNG 8

## RESULT 76

US-08-646-301A-9/c  
; Sequence 9, Application US/08646301A  
; Patent No. 6194211  
; GENERAL INFORMATION:  
; APPLICANT: Richards, Cynthia Ann  
; APPLICANT: Huber, Brian E.  
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic  
; Patent No. 6194211  
; TITLE OF INVENTION: Antigen for Expression Targeting  
; FILE REFERENCE: FB1508USW  
; CURRENT APPLICATION NUMBER: US/08/646,301A  
; CURRENT FILING DATE: 1996-05-16  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: consensus  
; OTHER INFORMATION: sequence B2 from DNA Sequence 1:3-11 (1990).  
US-08-646-301A-9

Query Match 30.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWV 6  
|||  
Db 8 CWV 6

## RESULT 77

US-09-305-839-41  
; Sequence 41, Application US/09305839  
; Patent No. 6514935  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Mu-En  
; APPLICANT: Yet, Shaw-Fang  
; TITLE OF INVENTION: Methods of Treating Hypertension  
; FILE REFERENCE: 21508-064  
; CURRENT APPLICATION NUMBER: US/09/305,839  
; CURRENT FILING DATE: 1999-05-05  
; PRIOR APPLICATION NUMBER: 08/818,655  
; PRIOR FILING DATE: 1997-03-14  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: consensus  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: consensus  
US-09-305-839-41

Query Match 30.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
|||  
Db 6 YYY 8

## RESULT 78

US-09-305-839-41/c  
; Sequence 41, Application US/09305839  
; Patent No. 6514935  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Mu-En  
; APPLICANT: Yet, Shaw-Fang  
; TITLE OF INVENTION: Methods of Treating Hypertension  
; FILE REFERENCE: 21508-064  
; CURRENT APPLICATION NUMBER: US/09/305,839  
; CURRENT FILING DATE: 1999-05-05  
; PRIOR APPLICATION NUMBER: 08/818,655  
; PRIOR FILING DATE: 1997-03-14  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: consensus  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: consensus  
US-09-305-839-41

Query Match 30.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
|||  
Db 8 RRR 6

## RESULT 79

US-09-347-343-3  
; Sequence 3, Application US/09347343A  
; Patent No. 6514948  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eyal R.  
; APPLICANT: KOBAYASHI, Hiroko  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE  
; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/09/347,343A  
; CURRENT FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-09-347-343-3

Query Match 30.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
|||  
Db 1 RRC 3

## RESULT 80

US-09-347-343-3/c  
; Sequence 3, Application US/09347343A  
; Patent No. 6514948  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eyal R.  
; APPLICANT: KOBAYASHI, Hiroko  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE  
; FILE REFERENCE: 30448.64US01  
US-09-347-343-3

; CURRENT APPLICATION NUMBER: US/09/347,343A  
; CURRENT FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-09-347-343-3

Query Match 30.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
|||  
Db 6 RRC 4

RESULT 81  
US-09-347-343-4  
; Sequence 4, Application US/09347343A  
; Patent No. 6514948  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eyal R.  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE  
; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/09/347,343A  
; CURRENT FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-09-347-343-4

Query Match 30.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9  
|||  
Db 4 GY 6

RESULT 82  
US-09-347-343-4/c  
; Sequence 4, Application US/09347343A  
; Patent No. 6514948  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eyal R.  
; APPLICANT: KOBAYASHI, Hiroko  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE  
; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/09/347,343A  
; CURRENT FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-09-347-343-4

Query Match 30.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
|||  
Db 6 RRC 4

RESULT 83  
US-09-263-692A-7  
; Sequence 7, Application US/09263692A  
; Patent No. 6639065  
; GENERAL INFORMATION:  
; APPLICANT: Council of Scientific and Industrial Research  
; TITLE OF INVENTION: A chemically synthesized artificial promoter for high level expression of transgenes and a method for its synthesis  
; FILE REFERENCE: Q52511  
; CURRENT APPLICATION NUMBER: US/09/263,692A  
; CURRENT FILING DATE: 1999-03-05  
; PRIOR APPLICATION NUMBER: 3322/Del/98  
; PRIOR FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: domain II(a)  
US-09-263-692A-7

Query Match 30.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
|||  
Db 1 RRR 3

RESULT 84  
US-09-263-692A-7/c  
; Sequence 7, Application US/09263692A  
; Patent No. 6639065  
; GENERAL INFORMATION:  
; APPLICANT: Council of Scientific and Industrial Research  
; TITLE OF INVENTION: A chemically synthesized artificial promoter for high level expression of transgenes and a method for its synthesis  
; FILE REFERENCE: Q52511  
; CURRENT APPLICATION NUMBER: US/09/263,692A  
; CURRENT FILING DATE: 1999-03-05  
; PRIOR APPLICATION NUMBER: 3322/Del/98  
; PRIOR FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: domain II(a)  
US-09-263-692A-7

Query Match 30.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
|||  
Db 8 YYY 6

RESULT 85  
US-07-882-838E-1  
; Sequence 1, Application US/07882838E  
; Patent No. 5616461  
; GENERAL INFORMATION:  
; APPLICANT: Priscilla A. Schaffer  
; APPLICANT: Christine E. Dabrowski Amaral

```

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; STREET: One Liberty Place
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/882,838E
; FILING DATE: May 14, 1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kathryn Leary
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: DFCI-0001
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-882-838E-1
;
; Query Match 30.0%; Score 3; DB 1; Length 9;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 8 YYY 10
Db 4 YYY 6
;
; RESULT 86
; US-07-882-838E-1/c
; Sequence 1, Application US/07882838E
; Patent No. 5616461
; GENERAL INFORMATION:
; APPLICANT: Priscilla A. Schaffer
; APPLICANT: Christine E. Dabrowski Amarel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; STREET: One Liberty Place
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/882,838E
; FILING DATE: May 14, 1992
; CLASSIFICATION: 435

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kathryn Leary
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: DFCI-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-882-838E-1
;
; Query Match 30.0%; Score 3; DB 1; Length 9;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 RRR 3
Db 6 RRR 4
;
; RESULT 87
; US-08-643-886-11
; Sequence 11, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-761-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
; US-08-643-886-11
;
; Query Match 30.0%; Score 3; DB 1; Length 9;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 RRR 3  
Db 6 RRR 8

RESULT 88  
US-08-643-886-11/c  
; Sequence 11, Application US/08643886  
; Patent No. 5695977  
; GENERAL INFORMATION:  
; APPLICANT: JURKA, Jerzy W.  
; TITLE OF INVENTION: Site Directed Recombination  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/643,886  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rowland, Bertram I  
; REGISTRATION NUMBER: 20015  
; REFERENCE/DOCKET NUMBER: A-63252/BIR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "sequence"  
US-08-643-886-11

Query Match 30.0%; Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 8 YYY 6

RESULT 89  
US-08-122-433-34  
; Sequence 34, Application US/08122433  
; Patent No. 5683985  
; GENERAL INFORMATION:  
; APPLICANT: Chu, Barbara C.F.  
; APPLICANT: Orgel, Leslie  
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND  
; TITLE OF INVENTION: OLIGONUCLEOTIDES USEFUL AS DECOYS FOR PROTEINS WHICH  
; TITLE OF INVENTION: SELECTIVELY BIND TO DEFINED DNA SEQUENCES  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/122,433  
; FILING DATE: 22-SEP-1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/687,337  
; FILING DATE: 18-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P31 9308  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-1995  
; TELEFAX: 619-546-9392  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
US-08-122-433-34

Query Match 30.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6  
Db 2 CWW 4

RESULT 90  
US-08-122-433-34/c  
; Sequence 34, Application US/08122433  
; Patent No. 5683985  
; GENERAL INFORMATION:  
; APPLICANT: Chu, Barbara C.F.  
; APPLICANT: Orgel, Leslie  
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND  
; TITLE OF INVENTION: OLIGONUCLEOTIDES USEFUL AS DECOYS FOR PROTEINS WHICH  
; TITLE OF INVENTION: SELECTIVELY BIND TO DEFINED DNA SEQUENCES  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/122,433  
; FILING DATE: 22-SEP-1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/687,337  
; FILING DATE: 18-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P31 9308  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-546-1995

TELEFAX: 619-546-9392  
 INFORMATION FOR SEQ ID NO: 34:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 US-08-122-433-34

Query Match 30.0%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6  
 Db 9 CWW 7

## RESULT 91

US-08-643-886-1  
 Sequence 1, Application US/08643886  
 Patent No. 5695977  
 GENERAL INFORMATION:  
 APPLICANT: JURKA, Jerzy W.  
 TITLE OF INVENTION: Site Directed Recombination  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: US  
 ZIP: 94111

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/643,886  
 FILING DATE:

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rowland, Bertram I  
 REGISTRATION NUMBER: 20015  
 REFERENCE/DOCKET NUMBER: A-63252/BIR  
 TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "sequence"

US-08-643-886-1  
 Query Match 30.0%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
 Db 7 YYY 9

## RESULT 92

US-08-643-886-1/c  
 Sequence 1, Application US/08643886  
 Patent No. 5695977

GENERAL INFORMATION:  
 APPLICANT: JURKA, Jerzy W.  
 TITLE OF INVENTION: Site Directed Recombination  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: US  
 ZIP: 94111

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/643,886  
 FILING DATE:

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rowland, Bertram I  
 REGISTRATION NUMBER: 20015  
 REFERENCE/DOCKET NUMBER: A-63252/BIR  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "sequence"

US-08-643-886-1  
 Query Match 30.0%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
 Db 9 RRR 7

## RESULT 93

US-08-643-886-12  
 Sequence 12, Application US/08643886  
 Patent No. 5695977  
 GENERAL INFORMATION:

APPLICANT: JURKA, Jerzy W.  
 TITLE OF INVENTION: Site Directed Recombination  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: US  
 ZIP: 94111

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/643,886  
 FILING DATE:

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rowland, Bertram I  
 REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-63252/BIR  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "sequence"  
US-08-643-886-12

Query Match 30.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
|||  
Db 7 RRR 9

RESULT 94  
US-08-643-886-12/c  
Sequence 12, Application US/08643886  
Patent No. 5695977  
GENERAL INFORMATION:  
APPLICANT: JURKA, Jerzy W.  
TITLE OF INVENTION: Site Directed Recombination  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/643,886  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I  
REGISTRATION NUMBER: 20015  
REFERENCE/DOCKET NUMBER: A-63252/BIR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "sequence"  
US-08-643-886-12

Query Match 30.0%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
|||  
Db 9 YYY 7

RESULT 95  
US-08-472-809B-5  
Sequence 5, Application US/08472809B  
Patent No. 5925564  
GENERAL INFORMATION:  
APPLICANT: Schwartz, Robert J.  
APPLICANT: DeMayo, Franco J.  
APPLICANT: O'Malley, Bert W.  
TITLE OF INVENTION: Expression Vector Systems and  
METHOD OF INVENTION: Method of Use  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,809B  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/209,846  
FILING DATE: March 9, 1994  
APPLICATION NUMBER: 07/789,919  
FILING DATE: No. 5925564member 6, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 214/212  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
OTHER INFORMATION: /note= W = A or T  
US-08-472-809B-5  
Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 CWW 6  
|||  
Db 2 CWW 4  
|||  
RESULT 96  
US-08-472-809B-5/c  
Sequence 5, Application US/08472809B  
Patent No. 5925564  
GENERAL INFORMATION:  
APPLICANT: Schwartz, Robert J.  
APPLICANT: DeMayo, Franco J.  
APPLICANT: O'Malley, Bert W.  
TITLE OF INVENTION: Expression Vector Systems and  
METHOD OF INVENTION: Method of Use  
NUMBER OF SEQUENCES: 8

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/472,809B
/ FILING DATE: June 7, 1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/209,846
/ FILING DATE: March 9, 1994
/ APPLICATION NUMBER: 07/789,919
/ FILING DATE: No. 5925564ember 6, 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 214/212
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 5:
/ LENGTH: 10 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ OTHER INFORMATION: /note= W = A or T
/
US-08-472-809B-5

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWX 6
Db 9 CWX 7

RESULT 97
US-08-481-658B-23
/ Sequence 23, Application US/08481658B
/ Patent No. 5955075
/ GENERAL INFORMATION:
/ APPLICANT: Zavada, Jan
/ APPLICANT: Pastorekova, Silvia
/ TITLE OF INVENTION: MN Gene and Protein
/ NUMBER OF SEQUENCES: 86
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Leona L. Lauder
/ STREET: 6 Mariposa Court
/ CITY: Tiburon
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94920
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,658B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/260,190
/ FILING DATE: 15-JUN-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lauder, Leona L.
/ REGISTRATION NUMBER: 30,863
/ REFERENCE/DOCKET NUMBER: D-0021.3E
/ TELEPHONE: 415-435-2034
/ TELEFAX: 415-435-0727
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
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/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,658B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/260,190
/ FILING DATE: 15-JUN-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lauder, Leona L.
/ REGISTRATION NUMBER: 30,863
/ REFERENCE/DOCKET NUMBER: D-0021.3E
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-435-2034
/ TELEFAX: 415-435-0727
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ DESCRIPTION: Initiator consensus sequence
/
US-08-481-658B-23

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
Db 1 YYY 3

RESULT 98
US-08-481-658B-23/c
/ Sequence 23, Application US/08481658B
/ Patent No. 5955075
/ GENERAL INFORMATION:
/ APPLICANT: Zavada, Jan
/ APPLICANT: Pastorekova, Silvia
/ TITLE OF INVENTION: MN Gene and Protein
/ NUMBER OF SEQUENCES: 86
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Leona L. Lauder
/ STREET: 6 Mariposa Court
/ CITY: Tiburon
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94920
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,658B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/260,190
/ FILING DATE: 15-JUN-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lauder, Leona L.
/ REGISTRATION NUMBER: 30,863
/ REFERENCE/DOCKET NUMBER: D-0021.3E
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-435-2034
/ TELEFAX: 415-435-0727
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
```



STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: Initiator consensus sequence  
US-08-481-658B-23

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 10 RRR 8

RESULT 99  
US-08-477-504A-23  
; Sequence 23, Application US/08477504A  
; Patent No. 5972353

GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,504A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: Initiator consensus sequence  
US-08-477-504A-23

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 1 YYY 3

RESULT 100  
US-08-477-504A-23/c  
; Sequence 23, Application US/08477504A

Patent No. 5972353  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,504A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: Initiator consensus sequence  
US-08-477-504A-23

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 10 RRR 8

RESULT 101  
US-08-486-756A-23  
; Sequence 23, Application US/08486756A  
; Patent No. 5981711

GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

;  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,756A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-435-2034  
; TELEFAX: 415-435-0727  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Initiator consensus sequence  
; US-08-486-756A-23

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
|||  
Db 1 YYY 3

RESULT 102  
US-08-486-756A-23/c  
; Sequence 23, Application US/08486756A  
; Patent No. 5981711  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,756A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-435-2034  
; TELEFAX: 415-435-0727  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs

;  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Initiator consensus sequence  
; US-08-486-756A-23

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
|||  
Db 10 RRR 8

RESULT 103  
US-08-485-862B-23  
; Sequence 23, Application US/08485862B  
; Patent No. 5989838  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,862B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/477,504  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-435-2034  
; TELEFAX: 415-435-0727  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Initiator consensus sequence  
; US-08-485-862B-23

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
|||  
Db 1 YYY 3

## RESULT 104

US-08-485-862B-23/c  
; Sequence 23, Application US/08485862B  
; Patent No. 5989838  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485.862B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/477,504  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-435-2034  
; TELEFAX: 415-435-0727  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Initiator consensus sequence  
US-08-485-862B-23

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 10 RRR 8

## RESULT 105

US-08-787-739-23  
; Sequence 23, Application US/08787739  
; Patent No. 6027887  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street, Suite 610  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104

ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/787,739  
; FILING DATE: 24-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/486,756  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/477,504  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/481,658  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,862  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/485,863  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/487,077  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Initiator consensus sequence  
US-08-787-739-23

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 1 YYY 3

## RESULT 106

US-08-787-739-23/c  
; Sequence 23, Application US/08787739  
; Patent No. 6027887  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street, Suite 610  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)  
CURRENT APPLICATION NUMBER: US/08/787,739  
FILING DATE: 24-JAN-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,049  
FILING DATE: 07-JUN-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,756  
FILING DATE: 07-JUN-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/477,504  
FILING DATE: 07-JUN-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/481,658  
FILING DATE: 07-JUN-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,862  
FILING DATE: 07-JUN-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,863  
FILING DATE: 07-JUN-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,077  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-981-2034  
TELEFAX: 415-981-0332  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: Initiator consensus sequence  
US-08-787-739-23

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 10 RRR 8

RESULT 107  
US-08-742-877-13  
Sequence 13, Application US/08742877  
Patent No. 6046380  
GENERAL INFORMATION:  
APPLICANT: CLARK, Anthony J.  
TITLE OF INVENTION: DNA SEQUENCES  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/742,877  
FILING DATE: 01-NOV-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9408717.8  
FILING DATE: 03-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FLESHNER, RAZ E.  
REGISTRATION NUMBER: 34,331  
REFERENCE/DOCKET NUMBER: 0623.0470001/REF  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/742,877  
FILING DATE: 01-NOV-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9408717.8  
FILING DATE: 03-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FLESHNER, RAZ E.  
REGISTRATION NUMBER: 34,331  
REFERENCE/DOCKET NUMBER: 0623.0470001/REF  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: mRNA  
US-08-742-877-13

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 1 YYY 3

RESULT 108  
US-08-742-877-13/c  
Sequence 13, Application US/08742877  
Patent No. 6046380  
GENERAL INFORMATION:  
APPLICANT: CLARK, Anthony J.  
TITLE OF INVENTION: DNA SEQUENCES  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/742,877  
FILING DATE: 01-NOV-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9408717.8  
FILING DATE: 03-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FLESHNER, RAZ E.  
REGISTRATION NUMBER: 34,331  
REFERENCE/DOCKET NUMBER: 0623.0470001/REF  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: mRNA  
US-08-742-877-13

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 6 RRR 4

## RESULT 109

US-08-487-077A-23

; Sequence 23, Application US/08487077A

; Patent No. 6069242

; GENERAL INFORMATION:

; APPLICANT: Zavada, Jan

; APPLICANT: Pastorekova, Silvia

; APPLICANT: Pastorek, Jaromir

; TITLE OF INVENTION: MN Gene and Protein

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leona L. Lauder

; STREET: 6 Mariposa Court

; CITY: Tiburon

; STATE: California

; COUNTRY: USA

; ZIP: 94920

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,077A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/260,190

; FILING DATE: 15-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lauder, Leona L.

; REGISTRATION NUMBER: 30,863

; REFERENCE/DOCKET NUMBER: D-0021.3H

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-435-2034

; TELEFAX: 415-435-0727

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; DESCRIPTION: Initiator consensus sequence

US-08-487-077A-23

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 1 YYY 3

## RESULT 110

US-08-487-077A-23/c

; Sequence 23, Application US/08487077A

; Patent No. 6069242

; GENERAL INFORMATION:

; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,077A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/260,190

; FILING DATE: 15-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lauder, Leona L.

; REGISTRATION NUMBER: 30,863

; REFERENCE/DOCKET NUMBER: D-0021.3H

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-435-2034

; TELEFAX: 415-435-0727

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; DESCRIPTION: Initiator consensus sequence

US-08-487-077A-23

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 10 RRR 8

## RESULT 111

US-08-726-807B-47

; Sequence 47, Application US/08726807B

; Patent No. 6090618

; GENERAL INFORMATION:

; APPLICANT: Farmacek, Michael S.

; APPLICANT: Solway, Julian

; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White &amp; Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,807B  
FILING DATE: 07-OCT-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/004,868  
FILING DATE: 05-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabeela R.  
REGISTRATION NUMBER: P-43,363  
REFERENCE/DOCKET NUMBER: ARSB:510  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 3..8  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "W = A or T"  
US-08-726-807B-47

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWW 6  
DB 2 CWW 4

## RESULT 112

US-08-726-807B-47/c  
Sequence 47, Application US/08726807B  
Patent No. 6090618  
GENERAL INFORMATION:  
APPLICANT: Parmacek, Michael S.  
APPLICANT: Solway, Julian  
TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,807B  
FILING DATE: 07-OCT-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/004,868  
FILING DATE: 05-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabeela R.  
REGISTRATION NUMBER: P-43,363  
REFERENCE/DOCKET NUMBER: ARSB:510  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 3..8  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "W = A or T"  
US-08-726-807B-47

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWG 7  
DB 4 WWG 2

## RESULT 113

US-08-485-863A-23  
Sequence 23, Application US/08485863A  
Patent No. 6093548  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,863A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3G  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: Initiator consensus sequence  
US-08-485-863A-23

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
DB 1 YYY 3

RESULT 114  
US-08-485-863A-23/c  
; Sequence 23, Application US/08485863A  
; Patent No. 6093548  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,863A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3G  
; TELEPHONE: 415-435-2034  
; TELEFAX: 415-435-0727  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Initiator consensus sequence  
US-08-485-863A-23  
  
Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RRR 3  
Db 10 RRR 8

RESULT 115  
US-09-258-367-47  
; Sequence 47, Application US/09258367  
; Patent No. 6114311  
; GENERAL INFORMATION:  
; APPLICANT: PARMACEK, MICHAEL S.  
; APPLICANT: SOLWAY, JULIAN  
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION  
; FILE REFERENCE: ARCD:310  
; CURRENT APPLICATION NUMBER: US/09/258,367  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 08/726,807  
; EARLIER FILING DATE: 1996-10-07  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 47

; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (3)..(8)  
; OTHER INFORMATION: W = A or T  
US-09-258-367-47  
  
Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 CWG 6  
Db 2 CWG 4

RESULT 116  
US-09-258-367-47/c  
; Sequence 47, Application US/09258367  
; Patent No. 6114311  
; GENERAL INFORMATION:  
; APPLICANT: PARMACEK, MICHAEL S.  
; APPLICANT: SOLWAY, JULIAN  
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION  
; FILE REFERENCE: ARCD:310  
; CURRENT APPLICATION NUMBER: US/09/258,367  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 08/726,807  
; EARLIER FILING DATE: 1996-10-07  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 47  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; FEATURE:  
; OTHER INFORMATION: Primer  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (3)..(8)  
; OTHER INFORMATION: W = A or T  
US-09-258-367-47  
  
Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 WWG 7  
Db 4 WWG 2

RESULT 117  
US-08-972-927-11  
; Sequence 11, Application US/08972927  
; Patent No. 6166290  
; GENERAL INFORMATION:  
; APPLICANT: Rea, Philip A  
; APPLICANT: Lu, Yu-Ping  
; APPLICANT: Li, Ze-Sheng  
; TITLE OF INVENTION: GLUTATHIONE-S-CONJUGATE TRANSPORT IN  
; TITLE OF INVENTION: PLANTS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: One Commerce Square, 2005 Market Street, 22nd  
; STREET: Floor

;  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: US  
; ZIP: 19103-7086  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/972,927  
; FILING DATE: 18-NOV-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/031,040  
; FILING DATE: 18-NOV-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/061,328  
; FILING DATE: 08-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Doyle Leary Ph.D., Kathryn  
; REGISTRATION NUMBER: 36,317  
; REFERENCE/DOCKET NUMBER: 9596-12U2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-567-2391  
; TELEX: 831-494  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-972-927-11  
  
Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 WWG 7  
Db 7 WWG 9  
  
RESULT 118  
US-08-972-927-11/c  
; Sequence 11, Application US/08972927  
; Patent No. 6166290  
; GENERAL INFORMATION:  
; APPLICANT: Rea, Philip A  
; APPLICANT: Lu, Yu-Ping  
; APPLICANT: Li, Ze-Sheng  
; TITLE OF INVENTION: GLUTATHIONE-S-CONJUGATE TRANSPORT IN  
; TITLE OF INVENTION: PLANTS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: One Commerce Square, 2005 Market Street, 22nd  
; STREET: Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: US  
; ZIP: 19103-7086  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/972,927  
; FILING DATE: 18-NOV-1997  
; CLASSIFICATION: 800

;  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/031,040  
; FILING DATE: 18-NOV-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/061,328  
; FILING DATE: 08-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Doyle Leary Ph.D., Kathryn  
; REGISTRATION NUMBER: 36,317  
; REFERENCE/DOCKET NUMBER: 9596-12U2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-965-1284  
; TELEX: 215-567-2991  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-972-927-11  
  
Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 CW 6  
Db 9 CW 7  
  
RESULT 119  
US-08-646-301A-11  
; Sequence 11, Application US/08646301A  
; Patent No. 6194211  
; GENERAL INFORMATION:  
; APPLICANT: Richards, Cynthia Ann  
; APPLICANT: Huber, Brian E.  
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic  
; TITLE OF INVENTION: Antigen for Expression Targeting  
; FILE REFERENCE: PB1508USW  
; CURRENT APPLICATION NUMBER: US/08/646,301A  
; CURRENT FILING DATE: 1996-05-16  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: consensus  
; OTHER INFORMATION: sequence B12 from DNA Sequence 1:3-11 (1990).  
; Patent No. 6194211  
US-08-646-301A-11  
  
Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 CW 6  
Db 2 CW 4  
  
RESULT 120  
US-08-646-301A-11/c  
; Sequence 11, Application US/08646301A  
; Patent No. 6194211  
; GENERAL INFORMATION:  
; APPLICANT: Richards, Cynthia Ann  
; APPLICANT: Huber, Brian E.



; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic  
; Patent No. 6194211  
; TITLE OF INVENTION: Antigen for Expression Targeting  
; FILE REFERENCE: PB1508USW  
; CURRENT APPLICATION NUMBER: US/08/646,301A  
; CURRENT FILING DATE: 1996-05-16  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: consensus  
; OTHER INFORMATION: sequence B12 from DNA Sequence 1:3-11 (1990).  
; Patent No. 6194211  
US-08-646-301A-11

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 6  
Db 9 CW 7

## RESULT 121

US-08-485-049D-23  
; Sequence 23, Application US/08485049D  
; Patent No. 6204370

GENERAL INFORMATION:

APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder

STREET: 369 Pine Street

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,049D

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.

REGISTRATION NUMBER: 30,863

REFERENCE/DOCKET NUMBER: D-0021.3E

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-981-2034

TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

DESCRIPTION: Initiator consensus sequence

US-08-485-049D-23

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
Db 1 YYY 3

## RESULT 122

US-08-485-049D-23/c

; Sequence 23, Application US/08485049D

; Patent No. 6204370

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder

STREET: 369 Pine Street

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,049D

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.

REGISTRATION NUMBER: 30,863

REFERENCE/DOCKET NUMBER: D-0021.3E

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-981-2034

TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

DESCRIPTION: Initiator consensus sequence

US-08-485-049D-23

Query Match 30.0%; Score 3; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
Db 10 RRR 8

## RESULT 123

US-09-134-246-1

; Sequence 1, Application US/09134246B

; Patent No. 6207377

GENERAL INFORMATION:

APPLICANT: Wayne, Jay

APPLICANT: Xu, Shuang-yong

TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle

TITLE OF INVENTION: Vectors And Identification of Two Thermus Plasmid

```
; TITLE OF INVENTION: Replication Origins
; FILE REFERENCE: Thermus Shuttle Vector
; CURRENT APPLICATION NUMBER: US/09/134,246B
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Thermus sp.
US-09-134-246-1

Query Match          30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RRC 4
Db      1 RRC 3

RESULT 124
US-09-134-246-1/c
; Sequence 1, Application US/09134246B
; Patent No. 6207377
; GENERAL INFORMATION:
; APPLICANT: Wayne, Jay
; TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
; TITLE OF INVENTION: Vectors And Identification Of Two Thermus plasmid
; TITLE OF INVENTION: Replication Origins
; FILE REFERENCE: Thermus Shuttle Vector
; CURRENT APPLICATION NUMBER: US/09/134,246B
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Thermus sp.
US-09-134-246-1

Query Match          30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
Db      10 RRR 8

RESULT 125
US-09-546-550-47
; Sequence 47, Application US/09546550
; Patent No. 6284743
; GENERAL INFORMATION:
; APPLICANT: PARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARCD:310
; CURRENT APPLICATION NUMBER: US/09/546,550
; CURRENT FILING DATE: 2000-04-10
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; OTHER INFORMATION: Primer
```

```
; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-546-550-47

Query Match          30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CWG 6
Db      2 CWG 4

RESULT 126
US-09-546-550-47/c
; Sequence 47, Application US/09546550
; Patent No. 6284743
; GENERAL INFORMATION:
; APPLICANT: PARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARCD:310
; CURRENT APPLICATION NUMBER: US/09/546,550
; CURRENT FILING DATE: 2000-04-10
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-546-550-47

Query Match          30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WVG 7
Db      4 WVG 2

RESULT 127
US-09-431-414-47
; Sequence 47, Application US/09431414
; Patent No. 6291211
; GENERAL INFORMATION:
; APPLICANT: PARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARCD:335
; CURRENT APPLICATION NUMBER: US/09/431,414
; CURRENT FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: 08/726,807
; PRIOR FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; OTHER INFORMATION: Primer
```





```
; OTHER INFORMATION: W = A or T
US-09-225-670-47

Query Match          30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CW 6
        |||
Db      2 CW 4

RESULT 134
US-09-225-670-47/c
; Sequence 47, Application US/09225670
; Patent No. 6297221
; GENERAL INFORMATION:
; APPLICANT: PHARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARSB:526
; CURRENT APPLICATION NUMBER: US/09/225,670
; CURRENT FILING DATE: 1999-01-05
; EARLIER FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-225-670-47

Query Match          30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WWG 7
        |||
Db      4 WWG 2

RESULT 135
US-09-431-349C-47
; Sequence 47, Application US/09431349C
; Patent No. 6331527
; GENERAL INFORMATION:
; APPLICANT: PHARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARSB:526
; CURRENT APPLICATION NUMBER: US/09/431,349C
; CURRENT FILING DATE: 1999-11-01
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: 09/225,670
; PRIOR FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-431-349C-47

Query Match          30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WWG 7
        |||
Db      4 WWG 2

RESULT 136
US-09-431-349C-47/c
; Sequence 47, Application US/09431349C
; Patent No. 6331527
; GENERAL INFORMATION:
; APPLICANT: PHARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARSB:526
; CURRENT APPLICATION NUMBER: US/09/431,349C
; CURRENT FILING DATE: 1999-11-01
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: 08/726,807
; PRIOR FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-431-349C-47

Query Match          30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WWG 7
        |||
Db      4 WWG 2

RESULT 137
US-09-122-171D-3
; Sequence 3, Application US/09122171D
; Patent No. 6423693
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Robert J.
; APPLICANT: Draghia-Akli, Ruxandra
; APPLICANT: Li, Xuyang
; APPLICANT: Eastman, Eric
; TITLE OF INVENTION: GHRH Expression System and Methods of Use
; FILE REFERENCE: 236/006 GeneMedicine
; CURRENT APPLICATION NUMBER: US/09/122,171D
; CURRENT FILING DATE: 1998-07-24
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 60/062,608
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: 60/053,609
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
```

; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: The inner core of the serum response element  
; NAME/KEY: misc.feature  
; LOCATION: (3)..(8)  
; OTHER INFORMATION: The letter "w" stands for a or t  
US-09-122-171D-3

Query Match 30.0%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6  
|||  
Db 2 CWW 4

RESULT 138  
US-09-122-171D-3/c  
; Sequence 3, Application US/09122171D  
; Patent No. 6423693  
; GENERAL INFORMATION:  
; APPLICANT: Schwartz, Robert J.  
; APPLICANT: Draghia-Akli, Ruxandra  
; APPLICANT: Li, Xuyang  
; APPLICANT: Eastman, Eric  
; TITLE OF INVENTION: GHRH Expression System and Methods of Use  
; FILE REFERENCE: 236/006 GeneMedicine  
; CURRENT APPLICATION NUMBER: US/09/122,171D  
; CURRENT FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 60/062,608  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: 60/053,609  
; PRIOR FILING DATE: 1997-07-24  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: The inner core of the serum response element  
; NAME/KEY: misc.feature  
; LOCATION: (3)..(8)  
; OTHER INFORMATION: The letter "w" stands for a or t  
US-09-122-171D-3

Query Match 30.0%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6  
|||  
Db 9 CWW 7

RESULT 139  
US-09-772-719B-23  
; Sequence 23, Application US/09772719B  
; Patent No. 6770438  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; Pastorekova, Silvia  
; Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 465 California Street, Suite 450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA

; Zip: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719B  
; FILING DATE: 30-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3A-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Initiator consensus sequence  
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-772-719B-23

Query Match 30.0%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
|||  
Db 1 YYY 3

RESULT 140  
US-09-772-719B-23/c  
; Sequence 23, Application US/09772719B  
; Patent No. 6770438  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; Pastorekova, Silvia  
; Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 465 California Street, Suite 450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; Zip: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719B  
; FILING DATE: 30-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3A-2

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-981-2034  
TELEFAX: 415-981-0332  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: Initiator consensus sequence  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-772-719B-23

Query Match 30.0%; Score 3; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
Db 10 RRR 8

## RESULT 141

5164316-1  
PATENT NO. 5164316  
APPLICANT: MCPHERSON, JOAN C.; KAY, ROBERT  
TITLE OF INVENTION: DNA CONSTRUCT FOR ENHANCING THE  
EFFICIENCY OF TRANSCRIPTION  
NUMBER OF SEQUENCES: 1  
CURRENT APPLICATION DATA:  
FILING DATE: 17-AUG-1989  
APPLICATION NUMBER: US/07/395,155  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 147,887  
FILING DATE: 25-JAN-1988  
APPLICATION NUMBER: 2,780  
FILING DATE: 13-JAN-1987  
SEQ ID NO: 1:  
LENGTH: 10  
5164316-1

Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWG 7  
Db 8 WWG 10

## RESULT 142

5164316-1/c  
PATENT NO. 5164316  
APPLICANT: MCPHERSON, JOAN C.; KAY, ROBERT  
TITLE OF INVENTION: DNA CONSTRUCT FOR ENHANCING THE  
EFFICIENCY OF TRANSCRIPTION  
NUMBER OF SEQUENCES: 1  
CURRENT APPLICATION DATA:  
FILING DATE: 17-AUG-1989  
APPLICATION NUMBER: US/07/395,155  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 147,887  
FILING DATE: 25-JAN-1988  
APPLICATION NUMBER: 2,780  
FILING DATE: 13-JAN-1987  
SEQ ID NO: 1:  
LENGTH: 10  
5164316-1

Query Match 30.0%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWG 6  
Db 10 CWG 8

## RESULT 143

US-08-643-886-13  
SEQUENCE 13, Application US/08643886  
PATENT NO. 5695977  
GENERAL INFORMATION:  
APPLICANT: JURKA, Jerzy W.  
TITLE OF INVENTION: Site Directed Recombination  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/643,886  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I  
REGISTRATION NUMBER: 20015  
REFERENCE/DOCKET NUMBER: A-63252/BIR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "sequence"  
US-08-643-886-13

Query Match 30.0%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
Db 8 RRR 10

## RESULT 144

US-08-643-886-13/c  
SEQUENCE 13, Application US/08643886  
PATENT NO. 5695977  
GENERAL INFORMATION:  
APPLICANT: JURKA, Jerzy W.  
TITLE OF INVENTION: Site Directed Recombination  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/643,886  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I  
REGISTRATION NUMBER: 20015  
REFERENCE/DOCKET NUMBER: A-63252/BIR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "sequence"  
US-08-643-886-13

Query Match 30.0%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
|||  
Db 10 YYY 8

RESULT 145  
US-08-643-886-2  
Sequence 2, Application US/08643886  
Patent No. 5695977  
GENERAL INFORMATION:  
APPLICANT: JURKA, Jerzy W.  
TITLE OF INVENTION: Site Directed Recombination  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/643,886  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I  
REGISTRATION NUMBER: 20015  
REFERENCE/DOCKET NUMBER: A-63252/BIR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "sequence"  
US-08-643-886-2

Query Match 30.0%; Score 3; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
|||  
Db 9 YYY 11

RESULT 146  
US-08-643-886-2/c  
Sequence 2, Application US/08643886  
Patent No. 5695977  
GENERAL INFORMATION:  
APPLICANT: JURKA, Jerzy W.  
TITLE OF INVENTION: Site Directed Recombination  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/643,886  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I  
REGISTRATION NUMBER: 20015  
REFERENCE/DOCKET NUMBER: A-63252/BIR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "sequence"  
US-08-643-886-2

Query Match 30.0%; Score 3; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
|||  
Db 11 RRR 9

RESULT 147  
US-08-643-886-14  
Sequence 14, Application US/08643886  
Patent No. 5695977  
GENERAL INFORMATION:  
APPLICANT: JURKA, Jerzy W.  
TITLE OF INVENTION: Site Directed Recombination  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA



; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/643,886  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rowland, Bertram I  
; REGISTRATION NUMBER: 20015  
; REFERENCE/DOCKET NUMBER: A-63252/BIR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "sequence"  
US-08-643-886-14

Query Match 30.0%; Score 3; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
DB 9 RRR 11

RESULT 148  
US-08-643-886-14/c  
; Sequence 14, Application US/08643886  
; Patent No. 5695977  
; GENERAL INFORMATION:  
; APPLICANT: JURKA, Jerzy W.  
; TITLE OF INVENTION: Site Directed Recombination  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/643,886  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rowland, Bertram I  
; REGISTRATION NUMBER: 20015  
; REFERENCE/DOCKET NUMBER: A-63252/BIR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "sequence"  
US-08-643-886-14

Query Match 30.0%; Score 3; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
DB 11 YYY 9

RESULT 149  
US-08-235-503B-33  
; Sequence 33, Application US/08235503B  
; Patent No. 5563036  
; GENERAL INFORMATION:  
; APPLICANT: Peterson, Michael G  
; APPLICANT: Baichwal, Vijay R  
; APPLICANT: Strulovici, Berta  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,503B  
; FILING DATE: 29-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: A-59332/RAO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-235-503B-33

Query Match 30.0%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
DB 11 YYY 13

RESULT 150  
US-08-235-503B-33/c  
; Sequence 33, Application US/08235503B  
; Patent No. 5563036  
; GENERAL INFORMATION:  
; APPLICANT: Peterson, Michael G  
; APPLICANT: Baichwal, Vijay R

```

/ APPLICANT: Strulovici, Berta
/ TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
/ NUMBER OF SEQUENCES: 75
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
/ STREET: 4 Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-4187
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/235,503B
/ FILING DATE: 29-APR-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Osman, Richard A.
/ REGISTRATION NUMBER: 36,627
/ REFERENCE/DOCKET NUMBER: A-59332/RAO
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ TELEX: 910 277299
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-235-503B-33

```

```

Query Match          30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 RRR 3
DB      13 RRR 11

```

```

RESULT 151
US-08-643-886-3
/ Sequence 3, Application US/08643886
/ Patent No. 5695977
/ GENERAL INFORMATION:
/ APPLICANT: JURKA, Jerzy W.
/ TITLE OF INVENTION: Site Directed Recombination
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: US
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/643,886
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Rowland, Bertram I
/ REGISTRATION NUMBER: 20015
/ REFERENCE/DOCKET NUMBER: A-63252/BIR

```

```

/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-781-1989
/ TELEFAX: 415-398-3249
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "sequence"
/ US-08-643-886-3

```

```

Query Match          30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 YYY 10
DB      10 YYY 12

```

```

RESULT 152
US-08-643-886-3/c
/ Sequence 3, Application US/08643886
/ Patent No. 5695977
/ GENERAL INFORMATION:
/ APPLICANT: JURKA, Jerzy W.
/ TITLE OF INVENTION: Site Directed Recombination
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: US
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/643,886
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Rowland, Bertram I
/ REGISTRATION NUMBER: 20015
/ REFERENCE/DOCKET NUMBER: A-63252/BIR
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-781-1989
/ TELEFAX: 415-398-3249
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "sequence"
/ US-08-643-886-3

```

```

Query Match          30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 RRR 3
DB      12 RRR 10

```

RESULT 153

```
US-08-643-886-15
; Sequence 15, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
;
US-08-643-886-15
Query Match 30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
   |||
Db 10 RRR 12

RESULT 154
US-08-643-886-15/c
; Sequence 15, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
;
US-08-643-886-15
Query Match 30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
   |||
Db 12 YYY 10

RESULT 155
PCT-US95-05265-33
; Sequence 33, Application PC/TUS9505265
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05265
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,503
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: PP-59232-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
;
PCT-US95-05265-33
Query Match 30.0%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 8 YY 10  
 Db 11 YY 13

RESULT 156  
 PCT-US95-05265-33/c  
 ; Sequence 32, Application PC/TUS9505265  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TULARIK, INC.  
 ; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY  
 ; NUMBER OF SEQUENCES: 74  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FLHR, HOHBACH, TEST, ALBRITTON & HERBERT  
 ; STREET: 4 Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/05265  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/235,503  
 ; FILING DATE: 29-APR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Osman, Richard A  
 ; REGISTRATION NUMBER: 36,627  
 ; REFERENCE/DOCKET NUMBER: FP-59232-PC/RAO  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 33:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 13 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cdna  
 ; PCT-US95-05265-33

Query Match 30.0%; Score 3; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
 Db 13 RRR 11

RESULT 157  
 US-07-882-838E-32  
 ; Sequence 32, Application US/07882838E  
 ; Patent No. 5616461  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Priscilla A. Schaffer  
 ; APPLICANT: Christine E. Dabrowski Amaral  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
 ; TREATMENT OF VIRUS INFECTIONS  
 ; NUMBER OF SEQUENCES: 49  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn  
 ; STREET: One Liberty Place  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.

ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX  
 ; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
 ; SOFTWARE: WordPerfect (Version 5.1)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/882,838E  
 ; FILING DATE: May 14, 1992  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kathryn Leary  
 ; REGISTRATION NUMBER: 36,317  
 ; REFERENCE/DOCKET NUMBER: DFCI-0001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-3100  
 ; TELEFAX: (215) 568-3439  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 32:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-07-882-838E-32

Query Match 30.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
 Db 8 RRC 10

RESULT 158  
 US-07-882-838E-32/c  
 ; Sequence 32, Application US/07882838E  
 ; Patent No. 5616461  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Priscilla A. Schaffer  
 ; APPLICANT: Christine E. Dabrowski Amaral  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
 ; TREATMENT OF VIRUS INFECTIONS  
 ; NUMBER OF SEQUENCES: 49  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn  
 ; STREET: One Liberty Place  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX  
 ; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
 ; SOFTWARE: WordPerfect (Version 5.1)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/882,838E  
 ; FILING DATE: May 14, 1992  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kathryn Leary  
 ; REGISTRATION NUMBER: 36,317  
 ; REFERENCE/DOCKET NUMBER: DFCI-0001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 32:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-07-882-838E-32

Query Match 30.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 9  
 |||  
 Db 10 GY 8

## RESULT 159

US-08-643-886-4  
 ; Sequence 4, Application US/08643886  
 ; Patent No. 5695977

GENERAL INFORMATION:  
 APPLICANT: JURKA, Jerzy W.  
 TITLE OF INVENTION: Site Directed Recombination  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: US  
 ZIP: 94111

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/643,886  
 FILING DATE:

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rowland, Bertram I  
 REGISTRATION NUMBER: 20015  
 REFERENCE/DOCKET NUMBER: A-63252/BIR

TELEPHONE: 415-781-1989  
 TELEFAX: 415-398-3249  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "sequence"

US-08-643-886-4

Query Match 30.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
 |||  
 Db 11 YYY 13

## RESULT 160

US-08-643-886-4/c  
 ; Sequence 4, Application US/08643886  
 ; Patent No. 5695977

GENERAL INFORMATION:  
 APPLICANT: JURKA, Jerzy W.  
 TITLE OF INVENTION: Site Directed Recombination  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: US  
 ZIP: 94111

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/643,886  
 FILING DATE:

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rowland, Bertram I  
 REGISTRATION NUMBER: 20015  
 REFERENCE/DOCKET NUMBER: A-63252/BIR

TELEPHONE: 415-781-1989  
 TELEFAX: 415-398-3249  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "sequence"

US-08-643-886-4

Query Match 30.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
 |||  
 Db 13 RRR 11

## RESULT 161

US-08-643-886-16  
 ; Sequence 16, Application US/08643886  
 ; Patent No. 5695977

GENERAL INFORMATION:  
 APPLICANT: JURKA, Jerzy W.  
 TITLE OF INVENTION: Site Directed Recombination  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: US  
 ZIP: 94111

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/643,886  
 FILING DATE:

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rowland, Bertram I  
 REGISTRATION NUMBER: 20015

/ REFERENCE/DOCKET NUMBER: A-63252/BIR  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 415-781-1989  
/ TELEFAX: 415-398-3249  
/ INFORMATION FOR SEQ ID NO: 16:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 14 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "sequence"  
US-08-643-886-16

Query Match 30.0%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 11 RRR 13

RESULT 162  
US-08-643-886-16/c  
/ Sequence 16, Application US/08643886  
/ Patent No. 5695977  
/ GENERAL INFORMATION:  
/ APPLICANT: JURKA, Jerzy W.  
/ TITLE OF INVENTION: Site Directed Recombination  
/ NUMBER OF SEQUENCES: 22  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
/ STREET: Four Embarcadero Center, Suite 3400  
/ CITY: San Francisco  
/ STATE: CA  
/ COUNTRY: US  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/643,886  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Rowland, Bertram I  
/ REGISTRATION NUMBER: 20015  
/ REFERENCE/DOCKET NUMBER: A-63252/BIR  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 415-781-1989  
/ TELEFAX: 415-398-3249  
/ INFORMATION FOR SEQ ID NO: 16:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 14 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "sequence"  
US-08-643-886-16

Query Match 30.0%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 13 YYY 11

RESULT 163  
US-08-646-789A-38  
/ Sequence 38, Application US/08646789A  
/ Patent No. 6022863  
/ GENERAL INFORMATION:  
/ APPLICANT: Peyman, John A.  
/ TITLE OF INVENTION: REGULATION OF GENE EXPRESSION  
/ NUMBER OF SEQUENCES: 101  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: PENNIE & EDMONDS  
/ STREET: 1155 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: U.S.A.  
/ ZIP: 10036-2711  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/646,789A  
/ FILING DATE: May 21, 1996  
/ CLASSIFICATION: 800  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Misrock, S. Leslie  
/ REGISTRATION NUMBER: 18,872  
/ REFERENCE/DOCKET NUMBER: 6523-006  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212) 790-9090  
/ TELEFAX: (212) 869-9741/8864  
/ TELEX: 66141 PENNIE  
/ INFORMATION FOR SEQ ID NO: 38:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 14 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA  
US-08-646-789A-38

Query Match 30.0%; Score 3; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 11 YYY 13

RESULT 164  
US-08-646-789A-38/c  
/ Sequence 38, Application US/08646789A  
/ Patent No. 6022863  
/ GENERAL INFORMATION:  
/ APPLICANT: Peyman, John A.  
/ TITLE OF INVENTION: REGULATION OF GENE EXPRESSION  
/ NUMBER OF SEQUENCES: 101  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: PENNIE & EDMONDS  
/ STREET: 1155 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: U.S.A.  
/ ZIP: 10036-2711  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/646,789A  
/ FILING DATE: May 21, 1996

```

; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-646-789A-38

Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
DB 14 RRR 12

RESULT 165
US-08-646-789A-39
; Sequence 39, Application US/08646789A
; Patent No. 6022863
; GENERAL INFORMATION:
; APPLICANT: Peyman, John A.
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,789A
; FILING DATE: May 21, 1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-646-789A-39

Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
DB 4 YYY 2

RESULT 167
US-08-646-301A-8
; Sequence 8, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
; APPLICANT: Richards, Cynthia Ann
; APPLICANT: Huber, Brian E.
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
; TITLE OF INVENTION: Antigen for Expression Targeting
; FILE REFERENCE: P61508USW
; CURRENT APPLICATION NUMBER: US/08/646,301A
; CURRENT FILING DATE: 1996-05-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
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/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: consensus
/ Patent No. 6194211
US-08-646-301A-8
Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 1 RRR 3

RESULT 168
US-08-646-301A-8/c
; Sequence 8, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
; APPLICANT: Richards, Cynthia Ann
; APPLICANT: Huber, Brian E.
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
; TITLE OF INVENTION: Antigen for Expression Targeting
; FILE REFERENCE: PB1508USW
; CURRENT APPLICATION NUMBER: US/08/646,301A
; CURRENT FILING DATE: 1996-05-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: consensus
/ Patent No. 6194211
US-08-646-301A-8
Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
Db 3 YYY 1

RESULT 169
US-09-305-639-7
; Sequence 7, Application US/09305639
; Patent No. 6200778
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Seiden, Richard F.
; TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
; FILE REFERENCE: 07236/016001
; CURRENT APPLICATION NUMBER: US/09/305,639
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: 60/084,663
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(14)
; OTHER INFORMATION: n = A,T,C or G
US-09-305-639-7
Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
Db 1 YYY 3

RESULT 170
US-09-305-639-7/c
; Sequence 7, Application US/09305639
; Patent No. 6200778
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Seiden, Richard F.
; TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
; FILE REFERENCE: 07236/016001
; CURRENT APPLICATION NUMBER: US/09/305,639
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: 60/084,663
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(14)
; OTHER INFORMATION: n = A,T,C or G
US-09-305-639-7
Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 10 RRR 8

RESULT 171
US-09-305-384-8
; Sequence 8, Application US/09305384
; Patent No. 6242218
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Seiden, Richard F.
; TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
; FILE REFERENCE: 07236/017001
; CURRENT APPLICATION NUMBER: US/09/305,384
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: US 60/084,649
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(14)
; OTHER INFORMATION: n = A,T,C or G
US-09-305-384-8
Query Match 30.0%; Score 3; DB 3; Length 14;
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```
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 YYY 10
      |||
Db      1 YYY 3

RESULT 172
US-09-305-384-8/c
; Sequence 8, Application US/09305384
; Patent No. 6242218
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
; FILE REFERENCE: 072367017001
; CURRENT APPLICATION NUMBER: US/09/305,384
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: US 60/084,649
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(14)
; OTHER INFORMATION: n = A,T,C or G
US-09-305-384-8

Query Match      30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRR 3
      |||
Db      10 RRR 8

RESULT 173
US-09-318-138-22
; Sequence 22, Application US/09318138
; Patent No. 6531123
; GENERAL INFORMATION:
; APPLICANT: CHANG, Lung-Ji
; TITLE OF INVENTION: LENTIVIRAL VECTORS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/318,138
; FILING DATE: 25-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/086,635
; FILING DATE: 26-MAY-1998
; APPLICATION NUMBER: US 08/935,312
; FILING DATE: 22-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: CHANG=109A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-318-138-22

Query Match      30.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 YYY 10
      |||
Db      1 YYY 3

US-09-318-138-22
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: CHANG=109A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-318-138-22

Query Match      30.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 YYY 10
      |||
Db      1 YYY 3

RESULT 174
US-09-318-138-22/c
; Sequence 22, Application US/09318138
; Patent No. 6531123
; GENERAL INFORMATION:
; APPLICANT: CHANG, Lung-Ji
; TITLE OF INVENTION: LENTIVIRAL VECTORS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/318,138
; FILING DATE: 25-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/086,635
; FILING DATE: 26-MAY-1998
; APPLICATION NUMBER: US 08/935,312
; FILING DATE: 22-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: CHANG=109A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-318-138-22

Query Match      30.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
|||  
Db 10 RRR 8

## RESULT 175

US-09-525-160B-10  
; Sequence 10, Application US/09525160B  
; Patent No. 6569681  
; GENERAL INFORMATION:  
; APPLICANT: Ivanov, Evguenii  
; TITLE OF INVENTION: METHODS OF IMPROVING HOMOLOGOUS RECOMBINATION  
; FILE REFERENCE: 10278/016001  
; CURRENT APPLICATION NUMBER: US/09/525,160B  
; CURRENT FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated oligonucleotide  
; NAME/KEY: misc\_feature  
; LOCATION: 11  
; OTHER INFORMATION: n = a, g, c or t  
US-09-525-160B-10

Query Match 30.0%; Score 3; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
|||  
Db 1 YYY 3

## RESULT 176

US-09-525-160B-10/c  
; Sequence 10, Application US/09525160B  
; Patent No. 6569681  
; GENERAL INFORMATION:  
; APPLICANT: Ivanov, Evguenii  
; TITLE OF INVENTION: METHODS OF IMPROVING HOMOLOGOUS RECOMBINATION  
; FILE REFERENCE: 10278/016001  
; CURRENT APPLICATION NUMBER: US/09/525,160B  
; CURRENT FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated oligonucleotide  
; NAME/KEY: misc\_feature  
; LOCATION: 11  
; OTHER INFORMATION: n = a, g, c or t  
US-09-525-160B-10

Query Match 30.0%; Score 3; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
|||  
Db 10 RRR 8

## RESULT 177

PCT-US94-06456-4  
; Sequence 4, Application PC/TUS9406456  
; GENERAL INFORMATION:  
; APPLICANT: Beutel, Bruce A.  
; APPLICANT: Coppola, George R.  
; APPLICANT: Sherman, Michael I.  
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC - DOS  
; SOFTWARE: DW4.V2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/06456  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/073,873  
; FILING DATE: 09-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olstein, Elliott M.  
; REGISTRATION NUMBER: 24,025  
; REFERENCE/DOCKET NUMBER: 23550-89  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: oligonucleotide  
; FEATURE:  
; OTHER INFORMATION: R is a modified or unmodified purine  
PCT-US94-06456-4

Query Match 30.0%; Score 3; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
|||  
Db 12 RRR 14

## RESULT 178

PCT-US94-06456-4/c  
; Sequence 4, Application PC/TUS9406456  
; GENERAL INFORMATION:  
; APPLICANT: Beutel, Bruce A.  
; APPLICANT: Coppola, George R.  
; APPLICANT: Sherman, Michael I.  
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
PCT-US94-06456-4

```
;
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; OTHER INFORMATION: R is a modified or unmodified purine
PCT-US94-06456-4

Query Match 30.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 14 YYY 12

RESULT 179
PCT-US94-06456-33
; Sequence 33, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; OTHER INFORMATION: R is a modified or unmodified purine.
PCT-US94-06456-33

Query Match 30.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 14 YYY 12

RESULT 179
PCT-US94-06456-33
; Sequence 33, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; OTHER INFORMATION: R is a modified or unmodified purine.
PCT-US94-06456-33

Query Match 30.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 14 YYY 12
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; OTHER INFORMATION: R is a modified or unmodified purine.
PCT-US94-06456-33

Query Match 30.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 12 RRR 14

RESULT 180
PCT-US94-06456-33/c
; Sequence 33, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; OTHER INFORMATION: R is a modified or unmodified purine.
PCT-US94-06456-33

Query Match 30.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 14 YYY 12
```

```
RESULT 181
US-08-643-886-5
; Sequence 5, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
;
US-08-643-886-5
Query Match 30.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
Db 12 YYY 14

RESULT 182
US-08-643-886-5/c
; Sequence 5, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
```

```
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
;
US-08-643-886-5
Query Match 30.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 14 RRR 12

RESULT 183
US-08-643-886-17
; Sequence 17, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
;
US-08-643-886-17
Query Match 30.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 RRR 3  
Db 12 RRR 14

## RESULT 184

US-08-643-886-17/c  
; Sequence 17, Application US/08643886  
; Patent No. 5695977  
; GENERAL INFORMATION:  
; APPLICANT: JURKA, Jerzy W.  
; TITLE OF INVENTION: Site Directed Recombination  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/643,886  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rowland, Bertram I  
; REGISTRATION NUMBER: 20015  
; REFERENCE/DOCKET NUMBER: A-63252/BIR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "sequence"

US-08-643-886-17

Query Match 30.0%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 14 YYY 12

## RESULT 185

US-08-737-371A-8  
; Sequence 8, Application US/08737371A  
; Patent No. 5959094  
; GENERAL INFORMATION:  
; APPLICANT: David WALLACH  
; APPLICANT: Peter KUHNERT  
; APPLICANT: Gotz EHRHARDT  
; APPLICANT: Oliver KEMPER  
; TITLE OF INVENTION: p75 TNF RECEPTOR PROMOTERS  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,371A  
; FILING DATE: 08-NOVEMBER-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05853  
; FILING DATE: 11-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 109,633  
; FILING DATE: 11-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH=14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

US-08-737-371A-8

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 1 YYY 3

## RESULT 186

US-08-737-371A-8/c  
; Sequence 8, Application US/08737371A  
; Patent No. 5959094  
; GENERAL INFORMATION:  
; APPLICANT: David WALLACH  
; APPLICANT: Peter KUHNERT  
; APPLICANT: Gotz EHRHARDT  
; APPLICANT: Oliver KEMPER  
; TITLE OF INVENTION: p75 TNF RECEPTOR PROMOTERS  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,371A  
; FILING DATE: 08-NOVEMBER-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05853  
; FILING DATE: 11-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 109,633  
; FILING DATE: 11-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.

/ REGISTRATION NUMBER: 25,618  
/ REFERENCE/DOCKET NUMBER: WALLACH=14  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-628-5197  
/ TELEFAX: 202-737-3528  
/ INFORMATION FOR SEQ ID NO: 8:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 15 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: cDNA  
US-08-737-371A-8

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
Db 11 RRR 9

RESULT 187  
US-08-256-004-4  
; Sequence 4, Application US/08256004  
; Patent No. 6001644  
; GENERAL INFORMATION:  
; APPLICANT: Robert J. Debs  
; APPLICANT: Ning Zhu  
; TITLE OF INVENTION: IN VIVO TRANSFECTION WITH A CFTR CODING  
; TITLE OF INVENTION: SEQUENCE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94306-2155

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,004  
; FILING DATE: August 22, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/11004

; FILING DATE: December 17, 1992  
; APPLICATION NUMBER: 07/972,135  
; FILING DATE: No. 6001644ember 5, 1992  
; APPLICATION NUMBER: 07/927,200  
; FILING DATE: August 6, 1992  
; APPLICATION NUMBER: 07/894,498  
; FILING DATE: June 4, 1992  
; APPLICATION NUMBER: 07/809,291  
; FILING DATE: December 17, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Neeley, Richard L.  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: UCSF-008/0005

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 843-5070  
; TELEFAX: (415) 857-0663  
; TELEX: 380816COOLEYPA  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15  
; TYPE: nucleic acid  
; STRANDEDNESS: single

US-08-737-371A-8

Query Match 30.0%; Score 3; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
Db 11 RRR 9

/ TOPOLOGY: linear  
US-08-256-004-4  
Query Match 30.0%; Score 3; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 YYY 10  
Db 1 YYY 3

RESULT 188  
US-08-256-004-4/c  
; Sequence 4, Application US/08256004  
; Patent No. 6001644  
; GENERAL INFORMATION:  
; APPLICANT: Robert J. Debs  
; APPLICANT: Ning Zhu  
; TITLE OF INVENTION: IN VIVO TRANSFECTION WITH A CFTR CODING  
; TITLE OF INVENTION: SEQUENCE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94306-2155

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,004  
; FILING DATE: August 22, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/11004

; FILING DATE: December 17, 1992  
; APPLICATION NUMBER: 07/972,135  
; FILING DATE: No. 6001644ember 5, 1992  
; APPLICATION NUMBER: 07/927,200  
; FILING DATE: August 6, 1992  
; APPLICATION NUMBER: 07/894,498  
; FILING DATE: June 4, 1992  
; APPLICATION NUMBER: 07/809,291  
; FILING DATE: December 17, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Neeley, Richard L.  
; REGISTRATION NUMBER: 30,092  
; REFERENCE/DOCKET NUMBER: UCSF-008/0005

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 843-5070  
; TELEFAX: (415) 857-0663  
; TELEX: 380816COOLEYPA  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-256-004-4

Query Match 30.0%; Score 3; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
Db 11 RRR 9

```
RESULT 189
US-09-461-686-3
; Sequence 3, Application US/09461686
; Patent No. 6620795
; GENERAL INFORMATION:
; APPLICANT: Debs, Robert J.
;           Zhu, Ning
; TITLE OF INVENTION: A Mammalian Transformation Complex
;           Comprising a Lipid Carrier and DNA Encoding CFTR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,686
; FILING DATE: 14-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,004
; FILING DATE: 22-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mycroft, Frank J.
; REGISTRATION NUMBER: 46,946
; REFERENCE/DOCKET NUMBER: 023070-064710US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-461-686-3
Query Match 30.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 190
US-09-461-686-3/C
; Sequence 3, Application US/09461686
; Patent No. 6620795
; GENERAL INFORMATION:
; APPLICANT: Debs, Robert J.
;           Zhu, Ning
; TITLE OF INVENTION: A Mammalian Transformation Complex
;           Comprising a Lipid Carrier and DNA Encoding CFTR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,686
; FILING DATE: 14-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,004
; FILING DATE: 22-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mycroft, Frank J.
; REGISTRATION NUMBER: 46,946
; REFERENCE/DOCKET NUMBER: 023070-064710US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-461-686-3
Query Match 30.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 10 RRR 8

RESULT 191
US-09-586-216C-5
; Sequence 5, Application US/09586216C
; Patent No. 6696272
; GENERAL INFORMATION:
; APPLICANT: MAHURAN, Don J.
; APPLICANT: CLARKE, Joe T.R.
; APPLICANT: CALLAHAN, John W.
; TITLE OF INVENTION: PRODUCTS AND METHODS FOR GAUCHER DISEASE THERAPY
; FILE REFERENCE: 24,131 USA
; CURRENT APPLICATION NUMBER: US/09/586,216C
; CURRENT FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/137,598
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 2,272,055
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc difference
; LOCATION: Y=1-10; n=11
; OTHER INFORMATION: y=c or u; n=any nucleotide
US-09-586-216C-5
Query Match 30.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3
```

RESULT 192  
US-09-586-216C-5/c  
; Sequence 5, Application US/09586216C  
; Patent No. 6696272  
; GENERAL INFORMATION:  
; APPLICANT: MAHURAN, Don J.  
; APPLICANT: CLARKE, Joe T.R.  
; APPLICANT: CALLAHAN, John W.  
; TITLE OF INVENTION: PRODUCTS AND METHODS FOR GAUCHER DISEASE THERAPY  
; FILE REFERENCE: 24,131 USA  
; CURRENT APPLICATION NUMBER: US/09/586,216C  
; CURRENT FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/137,598  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 2,272,055  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_difference  
; LOCATION: y=1-10; n=11  
; OTHER INFORMATION: y=c or u; n=any nucleotide  
US-09-586-216C-5

Query Match 30.0%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 10 RRR 8

RESULT 193  
PCT-US95-05853-8  
; Sequence 8, Application PC/TUS9505853  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: p75 TNF RECEPTOR PROMOTERS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05853  
; FILING DATE: 11-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 109,633  
; FILING DATE: 11-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH=14 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
PCT-US95-05853-8  
  
Query Match 30.0%; Score 3; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 1 YYY 3

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; Sequence 8, Application PC/TUS9505853  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: p75 TNF RECEPTOR PROMOTERS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05853  
; FILING DATE: 11-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 109,633  
; FILING DATE: 11-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH=14 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
PCT-US95-05853-8  
  
Query Match 30.0%; Score 3; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 11 RRR 9

RESULT 195  
US-08-486-421-32  
; Sequence 32, Application US/08486421  
; Patent No. 5672479  
; GENERAL INFORMATION:



APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,421  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,911  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-486-421-32  
Query Match 30.0%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RRR 3  
Db 13 RRR 15  
RESULT 196  
US-08-421-32/c  
Sequence 32, Application US/08486421  
Patent No. 5672479  
GENERAL INFORMATION:  
APPLICANT: Johnson, Edward M.  
APPLICANT: Bergemann, Andrew D.  
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,421  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,911  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6923-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-08-486-421-32  
Query Match 30.0%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 YYY 10  
Db 16 YYY 14  
RESULT 197  
US-08-643-886-6  
Sequence 6, Application US/08643886  
Patent No. 5695977  
GENERAL INFORMATION:  
APPLICANT: JURKA, Jerzy W.  
TITLE OF INVENTION: Site Directed Recombination  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/643,886  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I  
REGISTRATION NUMBER: 20015  
REFERENCE/DOCKET NUMBER: A-63252/BIR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
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US-08-643-886-6  
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Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
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Db 13 YYY 15

## RESULT 198

US-08-643-886-6/c  
; Sequence 6, Application US/08643886  
; Patent No. 5695977  
; GENERAL INFORMATION:  
; APPLICANT: JURKA, Jerzy W.  
; TITLE OF INVENTION: Site Directed Recombination  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/643,886  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rowland, Bertram I  
; REGISTRATION NUMBER: 20015  
; REFERENCE/DOCKET NUMBER: A-63252/BIR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "sequence"  
US-08-643-886-6

Query Match 30.0%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
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Db 15 RRR 13

## RESULT 199

US-08-643-886-18  
; Sequence 18, Application US/08643886  
; Patent No. 5695977  
; GENERAL INFORMATION:  
; APPLICANT: JURKA, Jerzy W.  
; TITLE OF INVENTION: Site Directed Recombination  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/643,886  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rowland, Bertram I  
; REGISTRATION NUMBER: 20015  
; REFERENCE/DOCKET NUMBER: A-63252/BIR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "sequence"  
US-08-643-886-18

Query Match 30.0%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
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Db 13 RRR 15

## RESULT 200

US-08-643-886-18/c  
; Sequence 18, Application US/08643886  
; Patent No. 5695977  
; GENERAL INFORMATION:  
; APPLICANT: JURKA, Jerzy W.  
; TITLE OF INVENTION: Site Directed Recombination  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/643,886  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rowland, Bertram I  
; REGISTRATION NUMBER: 20015  
; REFERENCE/DOCKET NUMBER: A-63252/BIR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "sequence"

US-08-643-886-18

Query Match 30.0%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YY 10  
|||  
Db 15 YY 13

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Job time : 89 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 17:06:55 ; Search time 399 Seconds  
(without alignments)  
144.007 Million cell updates/sec

Title: US-09-813-824A-3

Perfect score: 10

Sequence: 1 RRRCWGYY 10

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Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 90	4	40.0	30	18	US-10-658-093-52	Sequence 52, Appl	C 163	3	30.0	14	18	US-10-342-923-1	Sequence 1, Appl
C 91	4	40.0	38	9	US-09-179-536B-320	Sequence 320, App	C 164	3	30.0	14	18	US-10-342-923-1	Sequence 1, Appl
C 92	4	40.0	38	9	US-09-179-536B-320	Sequence 320, App	C 165	3	30.0	14	18	US-10-342-948-1	Sequence 1, Appl
C 93	4	40.0	38	10	US-09-297-576B-320	Sequence 320, App	C 166	3	30.0	14	18	US-10-342-948-1	Sequence 1, Appl
C 94	4	40.0	38	10	US-09-297-576B-320	Sequence 320, App	C 167	3	30.0	15	15	US-10-418-182-183	Sequence 183, App
C 95	3	30.0	4	17	US-10-293-252C-5	Sequence 5, Appl	C 168	3	30.0	15	15	US-10-418-182-183	Sequence 183, App
C 96	3	30.0	4	17	US-10-293-252C-5	Sequence 5, Appl	C 169	3	30.0	15	15	US-10-418-182-219	Sequence 219, App
C 97	3	30.0	4	17	US-10-340-861B-5	Sequence 5, Appl	C 170	3	30.0	15	15	US-10-418-182-219	Sequence 219, App
C 98	3	30.0	4	17	US-10-340-861B-5	Sequence 5, Appl	C 171	3	30.0	15	15	US-10-418-182-313	Sequence 313, App
C 99	3	30.0	6	15	US-10-253-117-1	Sequence 1, Appl	C 172	3	30.0	15	15	US-10-418-182-313	Sequence 313, App
C 100	3	30.0	6	15	US-10-253-117-1	Sequence 1, Appl	C 173	3	30.0	15	15	US-10-418-182-421	Sequence 421, App
C 101	3	30.0	6	15	US-10-253-117-2	Sequence 2, Appl	C 174	3	30.0	15	15	US-10-418-182-421	Sequence 421, App
C 102	3	30.0	6	15	US-10-253-117-2	Sequence 2, Appl	C 175	3	30.0	15	16	US-10-706-466-5	Sequence 5, Appl
C 103	3	30.0	6	15	US-10-290-545-27	Sequence 27, Appl	C 176	3	30.0	16	9	US-09-754-014-11	Sequence 11, Appl
C 104	3	30.0	6	15	US-10-290-545-27	Sequence 27, Appl	C 177	3	30.0	16	9	US-09-754-014-11	Sequence 11, Appl
C 105	3	30.0	6	16	US-10-437-263-27	Sequence 27, Appl	C 178	3	30.0	16	9	US-09-836-866-7	Sequence 7, Appl
C 106	3	30.0	6	16	US-10-437-263-27	Sequence 27, Appl	C 179	3	30.0	16	9	US-09-836-866-7	Sequence 7, Appl
C 107	3	30.0	6	16	US-10-437-275-27	Sequence 27, Appl	C 180	3	30.0	16	9	US-09-836-866-7	Sequence 7, Appl
C 108	3	30.0	6	16	US-10-437-275-27	Sequence 27, Appl	C 181	3	30.0	17	9	US-09-892-867-5	Sequence 5, Appl
C 109	3	30.0	6	16	US-10-437-275-27	Sequence 27, Appl	C 182	3	30.0	17	9	US-09-892-867-5	Sequence 5, Appl
C 110	3	30.0	6	16	US-10-437-258-27	Sequence 27, Appl	C 183	3	30.0	17	9	US-09-973-451-15	Sequence 15, Appl
C 111	3	30.0	8	9	US-09-816-763-16	Sequence 16, Appl	C 184	3	30.0	17	9	US-09-973-451-15	Sequence 15, Appl
C 112	3	30.0	8	9	US-09-816-763-16	Sequence 16, Appl	C 185	3	30.0	17	10	US-09-836-705-4	Sequence 4, Appl
C 113	3	30.0	8	9	US-09-816-763-32	Sequence 32, Appl	C 186	3	30.0	17	10	US-09-836-705-4	Sequence 4, Appl
C 114	3	30.0	8	9	US-09-816-763-32	Sequence 32, Appl	C 187	3	30.0	17	10	US-09-903-770-5	Sequence 5, Appl
C 115	3	30.0	8	10	US-09-798-883B-56	Sequence 56, Appl	C 188	3	30.0	17	10	US-09-903-770-5	Sequence 5, Appl
C 116	3	30.0	8	10	US-09-798-883B-56	Sequence 56, Appl	C 189	3	30.0	17	11	US-09-876-813-10	Sequence 10, Appl
C 117	3	30.0	8	10	US-09-326-885-56	Sequence 56, Appl	C 190	3	30.0	17	11	US-09-876-813-10	Sequence 10, Appl
C 118	3	30.0	8	10	US-09-326-885-56	Sequence 56, Appl	C 191	3	30.0	17	11	US-10-043-143-1	Sequence 1, Appl
C 119	3	30.0	8	15	US-10-253-117-3	Sequence 3, Appl	C 192	3	30.0	17	13	US-10-043-143-1	Sequence 1, Appl
C 120	3	30.0	8	15	US-10-253-117-3	Sequence 3, Appl	C 193	3	30.0	17	13	US-10-139-583-10	Sequence 10, Appl
C 121	3	30.0	8	15	US-10-253-117-3	Sequence 3, Appl	C 194	3	30.0	17	13	US-10-139-583-10	Sequence 10, Appl
C 122	3	30.0	8	15	US-10-253-117-4	Sequence 4, Appl	C 195	3	30.0	17	15	US-10-338-237-16	Sequence 16, Appl
C 123	3	30.0	8	15	US-10-253-117-4	Sequence 4, Appl	C 196	3	30.0	17	15	US-10-338-237-16	Sequence 16, Appl
C 124	3	30.0	8	17	US-10-821-568-32	Sequence 32, Appl	C 197	3	30.0	17	15	US-10-302-554-29	Sequence 29, Appl
C 125	3	30.0	8	17	US-10-821-568-32	Sequence 32, Appl	C 198	3	30.0	17	15	US-10-302-554-29	Sequence 29, Appl
C 126	3	30.0	10	9	US-09-772-719-23	Sequence 23, Appl	C 199	3	30.0	17	15	US-10-404-300A-28	Sequence 28, Appl
C 127	3	30.0	10	9	US-09-772-719-23	Sequence 23, Appl	C 200	3	30.0	17	15	US-10-404-300A-28	Sequence 28, Appl
C 128	3	30.0	10	10	US-09-967-237-23	Sequence 23, Appl	C 201	3	30.0	17	17	US-10-727-516-5	Sequence 5, Appl
C 129	3	30.0	10	10	US-09-967-237-23	Sequence 23, Appl	C 202	3	30.0	17	17	US-10-727-516-5	Sequence 5, Appl
C 130	3	30.0	10	14	US-10-124-759-3	Sequence 3, Appl	C 203	3	30.0	17	18	US-10-877-623-10	Sequence 10, Appl
C 131	3	30.0	10	14	US-10-124-759-3	Sequence 3, Appl	C 204	3	30.0	17	18	US-10-877-623-10	Sequence 10, Appl
C 132	3	30.0	10	16	US-10-338-587A-14	Sequence 14, Appl	C 205	3	30.0	18	15	US-10-274-095-46	Sequence 46, Appl
C 133	3	30.0	10	16	US-10-338-587A-14	Sequence 14, Appl	C 206	3	30.0	18	15	US-10-274-095-46	Sequence 46, Appl
C 134	3	30.0	10	16	US-10-172-526-15	Sequence 15, Appl	C 207	3	30.0	18	15	US-10-279-061-3	Sequence 3, Appl
C 135	3	30.0	10	16	US-10-172-526-15	Sequence 15, Appl	C 208	3	30.0	18	15	US-10-279-061-3	Sequence 3, Appl
C 136	3	30.0	10	18	US-10-689-006-32	Sequence 32, Appl	C 209	3	30.0	18	17	US-10-666-022-24	Sequence 24, Appl
C 137	3	30.0	10	18	US-10-689-006-32	Sequence 32, Appl	C 210	3	30.0	18	17	US-10-666-022-24	Sequence 24, Appl
C 138	3	30.0	10	18	US-10-888-694-23	Sequence 23, Appl	C 211	3	30.0	19	9	US-09-816-763-19	Sequence 19, Appl
C 139	3	30.0	12	15	US-10-359-050-3	Sequence 3, Appl	C 212	3	30.0	19	9	US-09-816-763-19	Sequence 19, Appl
C 140	3	30.0	12	15	US-10-359-050-3	Sequence 3, Appl	C 213	3	30.0	19	9	US-09-816-763-20	Sequence 20, Appl
C 141	3	30.0	12	15	US-10-359-050-4	Sequence 4, Appl	C 214	3	30.0	19	9	US-09-816-763-20	Sequence 20, Appl
C 142	3	30.0	12	15	US-10-359-050-4	Sequence 4, Appl	C 215	3	30.0	19	14	US-10-087-956-43	Sequence 43, Appl
C 143	3	30.0	12	15	US-10-359-050-4	Sequence 4, Appl	C 216	3	30.0	19	14	US-10-087-956-43	Sequence 43, Appl
C 144	3	30.0	12	15	US-10-300-011-78	Sequence 78, Appl	C 217	3	30.0	19	14	US-10-087-956-43	Sequence 43, Appl
C 145	3	30.0	12	15	US-10-300-011-78	Sequence 78, Appl	C 218	3	30.0	19	14	US-10-087-956-43	Sequence 43, Appl
C 146	3	30.0	13	9	US-09-816-763-67	Sequence 67, Appl	C 219	3	30.0	19	17	US-10-666-022-25	Sequence 25, Appl
C 147	3	30.0	13	9	US-09-816-763-67	Sequence 67, Appl	C 220	3	30.0	19	17	US-10-666-022-25	Sequence 25, Appl
C 148	3	30.0	13	16	US-10-602-837-15	Sequence 15, Appl	C 221	3	30.0	19	17	US-10-666-022-35	Sequence 35, Appl
C 149	3	30.0	13	16	US-10-602-837-15	Sequence 15, Appl	C 222	3	30.0	19	17	US-10-666-022-35	Sequence 35, Appl
C 150	3	30.0	13	17	US-10-821-568-67	Sequence 67, Appl	C 223	3	30.0	19	17	US-10-636-065-209	Sequence 209, App
C 151	3	30.0	13	17	US-10-821-568-67	Sequence 67, Appl	C 224	3	30.0	19	17	US-10-636-065-209	Sequence 209, App
C 152	3	30.0	14	9	US-09-802-807-7	Sequence 7, Appl	C 225	3	30.0	19	17	US-10-636-065-211	Sequence 211, App
C 153	3	30.0	14	10	US-09-845-020A-8	Sequence 8, Appl	C 226	3	30.0	19	17	US-10-821-568-19	Sequence 19, Appl
C 154	3	30.0	14	10	US-09-845-020A-8	Sequence 8, Appl	C 227	3	30.0	19	17	US-10-821-568-19	Sequence 19, Appl
C 155	3	30.0	14	15	US-10-345-115-1	Sequence 1, Appl	C 228	3	30.0	19	17	US-10-821-568-20	Sequence 20, Appl
C 156	3	30.0	14	15	US-10-345-115-1	Sequence 1, Appl	C 229	3	30.0	19	17	US-10-821-568-20	Sequence 20, Appl
C 157	3	30.0	14	16	US-10-277-612-1	Sequence 1, Appl	C 230	3	30.0	19	18	US-10-898-106-43	Sequence 43, Appl
C 158	3	30.0	14	16	US-10-277-612-1	Sequence 1, Appl	C 231	3	30.0	20	9	US-09-303-510-29	Sequence 29, Appl

C 232	20	9	US-09-303-510-29	Sequence 29, Appl	305	3	30.0	23	9	US-09-971-309-48	Sequence 48, Appl
C 233	3	30.0	US-10-243-501-4	Sequence 4, Appl	C 306	3	30.0	23	9	US-09-971-309-48	Sequence 48, Appl
C 234	20	14	US-10-243-501-4	Sequence 4, Appl	C 307	3	30.0	23	10	US-09-468-147-148	Sequence 148, App
C 235	20	14	US-10-243-351-3	Sequence 3, Appl	C 308	3	30.0	23	10	US-09-468-147-148	Sequence 148, App
C 236	20	14	US-10-243-351-3	Sequence 3, Appl	C 309	3	30.0	23	10	US-09-468-147-148	Sequence 148, App
C 237	20	15	US-10-273-051-19	Sequence 19, Appl	C 310	3	30.0	23	10	US-09-468-147-148	Sequence 148, App
C 238	20	15	US-10-273-051-19	Sequence 19, Appl	C 311	3	30.0	23	15	US-10-258-107-15	Sequence 15, Appl
C 239	20	15	US-10-404-300A-30	Sequence 30, Appl	C 312	3	30.0	23	15	US-10-258-107-15	Sequence 15, Appl
C 240	20	15	US-10-404-300A-30	Sequence 30, Appl	C 313	3	30.0	23	15	US-10-258-107-15	Sequence 15, Appl
C 241	20	15	US-10-129-518-19	Sequence 19, Appl	C 314	3	30.0	23	15	US-10-319-745-148	Sequence 148, App
C 242	20	15	US-10-129-518-19	Sequence 19, Appl	C 315	3	30.0	23	15	US-10-319-745-148	Sequence 148, App
C 243	20	16	US-10-338-110-54	Sequence 54, Appl	C 316	3	30.0	23	15	US-10-319-745-148	Sequence 148, App
C 244	20	16	US-10-338-110-54	Sequence 54, Appl	C 317	3	30.0	23	16	US-10-362-091-21	Sequence 21, Appl
C 245	20	17	US-10-666-022-26	Sequence 26, Appl	C 318	3	30.0	23	16	US-10-362-091-21	Sequence 21, Appl
C 246	20	17	US-10-666-022-26	Sequence 26, Appl	C 319	3	30.0	23	17	US-10-666-022-29	Sequence 29, Appl
C 247	20	17	US-10-666-022-26	Sequence 26, Appl	C 320	3	30.0	23	17	US-10-666-022-29	Sequence 29, Appl
C 248	20	17	US-10-666-022-36	Sequence 36, Appl	C 321	3	30.0	23	17	US-10-666-022-39	Sequence 39, Appl
C 249	20	17	US-10-666-022-36	Sequence 36, Appl	C 322	3	30.0	23	17	US-10-666-022-39	Sequence 39, Appl
C 250	20	17	US-10-666-022-46	Sequence 46, Appl	C 323	3	30.0	23	17	US-10-666-022-49	Sequence 49, Appl
C 251	20	17	US-10-666-022-46	Sequence 46, Appl	C 324	3	30.0	23	17	US-10-666-022-49	Sequence 49, Appl
C 252	20	17	US-10-666-022-101	Sequence 101, App	C 325	3	30.0	23	17	US-10-666-022-59	Sequence 59, Appl
C 253	20	17	US-10-666-022-101	Sequence 101, App	C 326	3	30.0	23	17	US-10-666-022-59	Sequence 59, Appl
C 254	20	17	US-10-641-665A-1	Sequence 1, Appl	C 327	3	30.0	23	17	US-10-666-022-59	Sequence 59, Appl
C 255	20	17	US-10-641-665A-1	Sequence 1, Appl	C 328	3	30.0	23	17	US-10-666-022-69	Sequence 69, Appl
C 256	20	17	US-10-641-665A-3	Sequence 3, Appl	C 329	3	30.0	23	17	US-10-666-022-69	Sequence 69, Appl
C 257	20	17	US-10-729-172-36	Sequence 36, Appl	C 330	3	30.0	23	17	US-10-666-022-79	Sequence 79, Appl
C 258	20	17	US-10-729-172-36	Sequence 36, Appl	C 331	3	30.0	23	17	US-10-666-022-79	Sequence 79, Appl
C 259	20	18	US-10-482-673-44	Sequence 44, Appl	C 332	3	30.0	23	17	US-10-666-022-104	Sequence 104, App
C 260	20	18	US-10-482-673-44	Sequence 44, Appl	C 333	3	30.0	23	17	US-10-666-022-104	Sequence 104, App
C 261	20	18	US-09-928-267-3	Sequence 3, Appl	C 334	3	30.0	23	17	US-10-666-022-114	Sequence 114, App
C 262	20	18	US-09-928-267-3	Sequence 3, Appl	C 335	3	30.0	23	17	US-10-666-022-114	Sequence 114, App
C 263	20	21	US-10-377-133-30	Sequence 30, Appl	C 336	3	30.0	23	17	US-10-666-022-124	Sequence 124, App
C 264	20	21	US-10-377-133-30	Sequence 30, Appl	C 337	3	30.0	23	17	US-10-666-022-124	Sequence 124, App
C 265	20	21	US-10-377-133-20	Sequence 20, Appl	C 338	3	30.0	23	17	US-10-666-022-134	Sequence 134, App
C 266	20	21	US-10-377-133-28	Sequence 28, Appl	C 339	3	30.0	23	17	US-10-666-022-134	Sequence 134, App
C 267	20	21	US-10-377-133-30	Sequence 30, Appl	C 340	3	30.0	23	17	US-10-637-544-11	Sequence 11, Appl
C 268	20	21	US-10-377-133-30	Sequence 30, Appl	C 341	3	30.0	23	17	US-10-637-544-11	Sequence 11, Appl
C 269	20	21	US-10-418-182-99	Sequence 99, Appl	C 342	3	30.0	24	9	US-09-785-632A-82	Sequence 82, Appl
C 270	20	21	US-10-418-182-99	Sequence 99, Appl	C 343	3	30.0	24	9	US-09-785-632A-82	Sequence 82, Appl
C 271	20	21	US-10-418-182-311	Sequence 311, App	C 344	3	30.0	24	15	US-10-278-087A-15	Sequence 15, Appl
C 272	20	21	US-10-418-182-311	Sequence 311, App	C 345	3	30.0	24	15	US-10-278-087A-15	Sequence 15, Appl
C 273	20	21	US-10-407-897-48	Sequence 48, Appl	C 346	3	30.0	24	15	US-10-080-263C-7	Sequence 7, Appl
C 274	20	21	US-10-407-897-48	Sequence 48, Appl	C 347	3	30.0	24	15	US-10-080-263C-7	Sequence 7, Appl
C 275	20	21	US-10-666-022-27	Sequence 27, Appl	C 348	3	30.0	24	15	US-10-223-765-82	Sequence 82, Appl
C 276	20	21	US-10-666-022-27	Sequence 27, Appl	C 349	3	30.0	24	15	US-10-223-765-82	Sequence 82, Appl
C 277	20	21	US-10-666-022-37	Sequence 37, Appl	C 350	3	30.0	24	17	US-10-666-022-30	Sequence 30, Appl
C 278	20	21	US-10-666-022-37	Sequence 37, Appl	C 351	3	30.0	24	17	US-10-666-022-30	Sequence 30, Appl
C 279	20	21	US-10-666-022-47	Sequence 47, Appl	C 352	3	30.0	24	17	US-10-666-022-40	Sequence 40, Appl
C 280	20	21	US-10-666-022-47	Sequence 47, Appl	C 353	3	30.0	24	17	US-10-666-022-50	Sequence 50, Appl
C 281	20	21	US-10-666-022-57	Sequence 57, Appl	C 354	3	30.0	24	17	US-10-666-022-50	Sequence 50, Appl
C 282	20	21	US-10-666-022-57	Sequence 57, Appl	C 355	3	30.0	24	17	US-10-666-022-60	Sequence 60, Appl
C 283	20	21	US-10-666-022-102	Sequence 102, App	C 356	3	30.0	24	17	US-10-666-022-60	Sequence 60, Appl
C 284	20	21	US-10-666-022-102	Sequence 102, App	C 357	3	30.0	24	17	US-10-666-022-70	Sequence 70, Appl
C 285	20	21	US-10-666-022-112	Sequence 112, App	C 358	3	30.0	24	17	US-10-666-022-70	Sequence 70, Appl
C 286	20	21	US-10-666-022-112	Sequence 112, App	C 359	3	30.0	24	17	US-10-666-022-80	Sequence 80, Appl
C 287	20	21	US-10-433-244-12	Sequence 12, Appl	C 360	3	30.0	24	17	US-10-666-022-80	Sequence 80, Appl
C 288	20	21	US-10-433-244-12	Sequence 12, Appl	C 361	3	30.0	24	17	US-10-666-022-90	Sequence 90, Appl
C 289	20	22	US-10-666-022-28	Sequence 28, Appl	C 362	3	30.0	24	17	US-10-666-022-90	Sequence 90, Appl
C 290	20	22	US-10-666-022-28	Sequence 28, Appl	C 363	3	30.0	24	17	US-10-666-022-105	Sequence 105, App
C 291	20	22	US-10-666-022-38	Sequence 38, Appl	C 364	3	30.0	24	17	US-10-666-022-105	Sequence 105, App
C 292	20	22	US-10-666-022-38	Sequence 38, Appl	C 365	3	30.0	24	17	US-10-666-022-115	Sequence 115, App
C 293	20	22	US-10-666-022-38	Sequence 38, Appl	C 366	3	30.0	24	17	US-10-666-022-115	Sequence 115, App
C 294	20	22	US-10-666-022-48	Sequence 48, Appl	C 367	3	30.0	24	17	US-10-666-022-125	Sequence 125, App
C 295	20	22	US-10-666-022-48	Sequence 48, Appl	C 368	3	30.0	24	17	US-10-666-022-125	Sequence 125, App
C 296	20	22	US-10-666-022-58	Sequence 58, Appl	C 369	3	30.0	24	17	US-10-666-022-135	Sequence 135, App
C 297	20	22	US-10-666-022-58	Sequence 58, Appl	C 370	3	30.0	24	17	US-10-666-022-135	Sequence 135, App
C 298	20	22	US-10-666-022-68	Sequence 68, Appl	C 371	3	30.0	24	17	US-10-666-022-145	Sequence 145, App
C 299	20	22	US-10-666-022-103	Sequence 103, App	C 372	3	30.0	24	17	US-10-666-022-145	Sequence 145, App
C 300	20	22	US-10-666-022-103	Sequence 103, App	C 373	3	30.0	24	18	US-10-770-824-78	Sequence 78, Appl
C 301	20	22	US-10-666-022-113	Sequence 113, App	C 374	3	30.0	24	18	US-10-770-824-78	Sequence 78, Appl
C 302	20	22	US-10-666-022-113	Sequence 113, App	C 375	3	30.0	25	17	US-10-666-022-31	Sequence 31, Appl
C 303	20	22	US-10-666-022-123	Sequence 123, App	C 376	3	30.0	25	17	US-10-666-022-31	Sequence 31, Appl
C 304	20	22	US-10-666-022-123	Sequence 123, App	C 377	3	30.0	25	17	US-10-666-022-41	Sequence 41, Appl

C 378	3	30.0	25	17	US-10-666-022-41	Sequence 41, Appl	451	3	30.0	27	15	US-10-037-986-337	Sequence 337, App
C 379	3	30.0	25	17	US-10-666-022-51	Sequence 51, Appl	C 452	3	30.0	27	15	US-10-037-986-337	Sequence 337, App
C 380	3	30.0	25	17	US-10-666-022-51	Sequence 51, Appl	C 452	3	30.0	27	15	US-10-251-686-4	Sequence 4, Appl1
C 381	3	30.0	25	17	US-10-666-022-61	Sequence 61, Appl	C 454	3	30.0	27	15	US-10-251-686-4	Sequence 4, Appl1
C 382	3	30.0	25	17	US-10-666-022-61	Sequence 61, Appl	C 454	3	30.0	27	15	US-10-223-666-268	Sequence 268, App
C 383	3	30.0	25	17	US-10-666-022-71	Sequence 71, Appl	C 456	3	30.0	27	15	US-10-223-666-268	Sequence 268, App
C 384	3	30.0	25	17	US-10-666-022-71	Sequence 71, Appl	C 457	3	30.0	27	15	US-10-408-085-337	Sequence 337, App
C 385	3	30.0	25	17	US-10-666-022-81	Sequence 81, Appl	C 458	3	30.0	27	15	US-10-408-085-337	Sequence 337, App
C 386	3	30.0	25	17	US-10-666-022-81	Sequence 81, Appl	C 459	3	30.0	27	15	US-10-132-067-11	Sequence 11, Appl
C 387	3	30.0	25	17	US-10-666-022-91	Sequence 91, Appl	C 460	3	30.0	27	15	US-10-132-067-11	Sequence 11, Appl
C 388	3	30.0	25	17	US-10-666-022-91	Sequence 91, Appl	C 461	3	30.0	27	15	US-10-167-634-3	Sequence 3, Appl1
C 389	3	30.0	25	17	US-10-666-022-91	Sequence 91, Appl	C 462	3	30.0	27	15	US-10-167-634-3	Sequence 3, Appl1
C 390	3	30.0	25	17	US-10-666-022-106	Sequence 106, App	C 463	3	30.0	27	15	US-10-418-182-155	Sequence 155, App
C 391	3	30.0	25	17	US-10-666-022-106	Sequence 106, App	C 463	3	30.0	27	15	US-10-418-182-155	Sequence 155, App
C 392	3	30.0	25	17	US-10-666-022-116	Sequence 116, App	C 464	3	30.0	27	15	US-10-418-182-157	Sequence 157, App
C 393	3	30.0	25	17	US-10-666-022-116	Sequence 116, App	C 465	3	30.0	27	15	US-10-418-182-157	Sequence 157, App
C 394	3	30.0	25	17	US-10-666-022-126	Sequence 126, App	C 466	3	30.0	27	15	US-10-418-182-354	Sequence 354, App
C 395	3	30.0	25	17	US-10-666-022-126	Sequence 126, App	C 467	3	30.0	27	15	US-10-418-182-354	Sequence 354, App
C 396	3	30.0	25	17	US-10-666-022-136	Sequence 136, App	C 468	3	30.0	27	15	US-10-418-182-354	Sequence 354, App
C 397	3	30.0	25	17	US-10-666-022-136	Sequence 136, App	C 469	3	30.0	27	15	US-10-418-182-360	Sequence 360, App
C 398	3	30.0	25	17	US-10-666-022-146	Sequence 146, App	C 470	3	30.0	27	15	US-10-418-182-360	Sequence 360, App
C 399	3	30.0	25	17	US-10-666-022-146	Sequence 146, App	C 471	3	30.0	27	16	US-10-418-182-360	Sequence 360, App
C 400	3	30.0	25	17	US-10-666-022-156	Sequence 156, App	C 472	3	30.0	27	16	US-10-418-251-52	Sequence 52, Appl
C 401	3	30.0	25	17	US-10-666-022-156	Sequence 156, App	C 473	3	30.0	27	16	US-10-418-251-52	Sequence 52, Appl
C 402	3	30.0	26	10	US-09-932-165-1498	Sequence 156, App	C 474	3	30.0	27	16	US-10-725-876-9	Sequence 9, Appl1
C 403	3	30.0	26	10	US-09-932-165-1498	Sequence 1498, Ap	C 475	3	30.0	27	16	US-10-725-876-9	Sequence 9, Appl1
C 404	3	30.0	26	10	US-09-932-165-1498	Sequence 1498, Ap	C 476	3	30.0	27	16	US-10-725-876-9	Sequence 9, Appl1
C 405	3	30.0	26	10	US-09-932-165-1499	Sequence 1499, Ap	C 477	3	30.0	27	16	US-10-725-876-9	Sequence 9, Appl1
C 406	3	30.0	26	15	US-10-037-986-343	Sequence 343, App	C 478	3	30.0	27	17	US-10-666-022-43	Sequence 43, Appl
C 407	3	30.0	26	15	US-10-037-986-343	Sequence 343, App	C 479	3	30.0	27	17	US-10-666-022-43	Sequence 43, Appl
C 408	3	30.0	26	15	US-10-223-666-269	Sequence 269, App	C 480	3	30.0	27	17	US-10-666-022-53	Sequence 53, Appl
C 409	3	30.0	26	15	US-10-223-666-269	Sequence 269, App	C 481	3	30.0	27	17	US-10-666-022-53	Sequence 53, Appl
C 410	3	30.0	26	15	US-10-408-085-343	Sequence 343, App	C 482	3	30.0	27	17	US-10-666-022-63	Sequence 63, Appl
C 411	3	30.0	26	15	US-10-408-085-343	Sequence 343, App	C 483	3	30.0	27	17	US-10-666-022-63	Sequence 63, Appl
C 412	3	30.0	26	15	US-10-364-839-8	Sequence 8, Appl1	C 484	3	30.0	27	17	US-10-666-022-73	Sequence 73, Appl
C 413	3	30.0	26	15	US-10-364-839-8	Sequence 8, Appl1	C 485	3	30.0	27	17	US-10-666-022-73	Sequence 73, Appl
C 414	3	30.0	26	17	US-10-666-022-32	Sequence 32, Appl	C 486	3	30.0	27	17	US-10-666-022-83	Sequence 83, Appl
C 415	3	30.0	26	17	US-10-666-022-32	Sequence 32, Appl	C 487	3	30.0	27	17	US-10-666-022-83	Sequence 83, Appl
C 416	3	30.0	26	17	US-10-666-022-42	Sequence 42, Appl	C 488	3	30.0	27	17	US-10-666-022-93	Sequence 93, Appl
C 417	3	30.0	26	17	US-10-666-022-42	Sequence 42, Appl	C 488	3	30.0	27	17	US-10-666-022-93	Sequence 93, Appl
C 418	3	30.0	26	17	US-10-666-022-52	Sequence 52, Appl	C 489	3	30.0	27	17	US-10-666-022-93	Sequence 93, Appl
C 419	3	30.0	26	17	US-10-666-022-52	Sequence 52, Appl	C 490	3	30.0	27	17	US-10-666-022-108	Sequence 108, App
C 420	3	30.0	26	17	US-10-666-022-52	Sequence 52, Appl	C 490	3	30.0	27	17	US-10-666-022-108	Sequence 108, App
C 421	3	30.0	26	17	US-10-666-022-62	Sequence 62, Appl	C 491	3	30.0	27	17	US-10-666-022-118	Sequence 118, App
C 422	3	30.0	26	17	US-10-666-022-62	Sequence 62, Appl	C 492	3	30.0	27	17	US-10-666-022-118	Sequence 118, App
C 423	3	30.0	26	17	US-10-666-022-72	Sequence 72, Appl	C 493	3	30.0	27	17	US-10-666-022-128	Sequence 128, App
C 424	3	30.0	26	17	US-10-666-022-72	Sequence 72, Appl	C 494	3	30.0	27	17	US-10-666-022-128	Sequence 128, App
C 425	3	30.0	26	17	US-10-666-022-82	Sequence 82, Appl	C 495	3	30.0	27	17	US-10-666-022-138	Sequence 138, App
C 426	3	30.0	26	17	US-10-666-022-82	Sequence 82, Appl	C 496	3	30.0	27	17	US-10-666-022-138	Sequence 138, App
C 427	3	30.0	26	17	US-10-666-022-92	Sequence 92, Appl	C 497	3	30.0	27	17	US-10-666-022-148	Sequence 148, App
C 428	3	30.0	26	17	US-10-666-022-92	Sequence 92, Appl	C 498	3	30.0	27	17	US-10-666-022-148	Sequence 148, App
C 429	3	30.0	26	17	US-10-666-022-107	Sequence 107, App	C 500	3	30.0	27	17	US-10-666-022-158	Sequence 158, App
C 430	3	30.0	26	17	US-10-666-022-117	Sequence 117, App	C 501	3	30.0	27	17	US-10-666-022-158	Sequence 158, App
C 431	3	30.0	26	17	US-10-666-022-117	Sequence 117, App	C 502	3	30.0	27	17	US-10-666-022-168	Sequence 168, App
C 432	3	30.0	26	17	US-10-666-022-127	Sequence 127, App	C 503	3	30.0	28	16	US-10-398-916-4	Sequence 4, Appl1
C 433	3	30.0	26	17	US-10-666-022-127	Sequence 127, App	C 504	3	30.0	28	16	US-10-398-916-4	Sequence 4, Appl1
C 434	3	30.0	26	17	US-10-666-022-137	Sequence 137, App	C 505	3	30.0	28	17	US-10-666-022-54	Sequence 54, Appl
C 435	3	30.0	26	17	US-10-666-022-137	Sequence 137, App	C 506	3	30.0	28	17	US-10-666-022-54	Sequence 54, Appl
C 436	3	30.0	26	17	US-10-666-022-147	Sequence 147, App	C 507	3	30.0	28	17	US-10-666-022-64	Sequence 64, Appl
C 437	3	30.0	26	17	US-10-666-022-147	Sequence 147, App	C 508	3	30.0	28	17	US-10-666-022-64	Sequence 64, Appl
C 438	3	30.0	26	17	US-10-666-022-157	Sequence 157, App	C 509	3	30.0	28	17	US-10-666-022-74	Sequence 74, Appl
C 439	3	30.0	26	17	US-10-666-022-157	Sequence 157, App	C 510	3	30.0	28	17	US-10-666-022-74	Sequence 74, Appl
C 440	3	30.0	26	17	US-10-666-022-167	Sequence 167, App	C 511	3	30.0	28	17	US-10-666-022-84	Sequence 84, Appl
C 441	3	30.0	26	17	US-10-666-022-167	Sequence 167, App	C 512	3	30.0	28	17	US-10-666-022-84	Sequence 84, Appl
C 442	3	30.0	26	18	US-10-815-480-4	Sequence 4, Appl1	C 513	3	30.0	28	17	US-10-666-022-94	Sequence 94, Appl
C 443	3	30.0	26	18	US-10-815-480-4	Sequence 4, Appl1	C 514	3	30.0	28	17	US-10-666-022-94	Sequence 94, Appl
C 444	3	30.0	27	9	US-09-780-651-7	Sequence 7, Appl1	C 515	3	30.0	28	17	US-10-666-022-109	Sequence 109, App
C 445	3	30.0	27	9	US-09-780-651-7	Sequence 7, Appl1	C 516	3	30.0	28	17	US-10-666-022-109	Sequence 109, App
C 446	3	30.0	27	9	US-09-780-651-8	Sequence 8, Appl1	C 517	3	30.0	28	17	US-10-666-022-119	Sequence 119, App
C 447	3	30.0	27	9	US-09-780-651-8	Sequence 8, Appl1	C 518	3	30.0	28	17	US-10-666-022-119	Sequence 119, App
C 448	3	30.0	27	14	US-10-001-546-59	Sequence 59, Appl	C 519	3	30.0	28	17	US-10-666-022-129	Sequence 129, App
C 449	3	30.0	27	14	US-10-001-546-59	Sequence 59, Appl	C 520	3	30.0	28	17	US-10-666-022-129	Sequence 129, App
C 450	3	30.0	27	14	US-10-001-546-60	Sequence 60, Appl	C 521	3	30.0	28	17	US-10-666-022-139	Sequence 139, App
C 451	3	30.0	27	14	US-10-001-546-60	Sequence 60, Appl	C 522	3	30.0	28	17	US-10-666-022-139	Sequence 139, App
							C 523	3	30.0	28	17	US-10-666-022-149	Sequence 149, App



c 524	3	30.0	28	17	US-10-666-022-149	Sequence 149, App	597	3	30.0	31	17	US-10-666-022-162	Sequence 162, App
c 525	3	30.0	28	17	US-10-666-022-159	Sequence 159, App	c 598	3	30.0	31	17	US-10-666-022-162	Sequence 162, App
c 526	3	30.0	28	17	US-10-666-022-159	Sequence 159, App	c 599	3	30.0	31	17	US-10-666-022-172	Sequence 172, App
c 527	3	30.0	28	17	US-10-666-022-169	Sequence 169, App	c 600	3	30.0	31	17	US-10-666-022-172	Sequence 172, App
c 528	3	30.0	28	17	US-10-666-022-169	Sequence 169, App	c 601	3	30.0	31	17	US-10-795-667-14	Sequence 14, Appl
c 529	3	30.0	28	18	US-10-795-667-11	Sequence 11, Appl	c 602	3	30.0	31	18	US-10-795-667-14	Sequence 14, Appl
c 530	3	30.0	28	18	US-10-795-667-11	Sequence 11, Appl	c 603	3	30.0	32	15	US-10-104-706-2	Sequence 2, Appl
c 531	3	30.0	28	18	US-10-257-047-53	Sequence 53, Appl	c 604	3	30.0	32	15	US-10-104-706-2	Sequence 2, Appl
c 532	3	30.0	28	18	US-10-257-047-53	Sequence 53, Appl	c 605	3	30.0	32	16	US-10-299-636-31	Sequence 31, Appl
c 533	3	30.0	29	9	US-09-813-781-104	Sequence 104, App	c 606	3	30.0	32	16	US-10-299-636-31	Sequence 31, Appl
c 534	3	30.0	29	9	US-09-813-781-104	Sequence 104, App	c 607	3	30.0	32	16	US-10-299-636-31	Sequence 31, Appl
c 535	3	30.0	29	15	US-10-037-986-342	Sequence 342, App	c 608	3	30.0	32	17	US-10-666-022-98	Sequence 98, Appl
c 536	3	30.0	29	15	US-10-037-986-342	Sequence 342, App	c 609	3	30.0	32	17	US-10-666-022-98	Sequence 98, Appl
c 537	3	30.0	29	15	US-10-408-085-342	Sequence 342, App	c 610	3	30.0	32	17	US-10-666-022-153	Sequence 153, App
c 538	3	30.0	29	15	US-10-408-085-342	Sequence 342, App	c 611	3	30.0	32	17	US-10-666-022-153	Sequence 153, App
c 539	3	30.0	29	16	US-10-355-238-15	Sequence 15, Appl	c 612	3	30.0	32	17	US-10-666-022-163	Sequence 163, App
c 540	3	30.0	29	16	US-10-355-238-15	Sequence 15, Appl	c 613	3	30.0	32	17	US-10-666-022-163	Sequence 163, App
c 541	3	30.0	29	17	US-10-666-022-65	Sequence 65, Appl	c 614	3	30.0	32	17	US-10-666-022-173	Sequence 173, App
c 542	3	30.0	29	17	US-10-666-022-65	Sequence 65, Appl	c 615	3	30.0	32	18	US-10-795-667-15	Sequence 15, Appl
c 543	3	30.0	29	17	US-10-666-022-75	Sequence 75, Appl	c 616	3	30.0	32	18	US-10-795-667-15	Sequence 15, Appl
c 544	3	30.0	29	17	US-10-666-022-75	Sequence 75, Appl	c 617	3	30.0	33	9	US-09-991-119-11	GENERAL INFORMA
c 545	3	30.0	29	17	US-10-666-022-85	Sequence 85, Appl	c 618	3	30.0	33	9	US-09-991-119-11	GENERAL INFORMA
c 546	3	30.0	29	17	US-10-666-022-85	Sequence 85, Appl	c 619	3	30.0	33	15	US-10-126-845-36	Sequence 36, Appl
c 547	3	30.0	29	17	US-10-666-022-95	Sequence 95, Appl	c 620	3	30.0	33	15	US-10-126-845-36	Sequence 36, Appl
c 548	3	30.0	29	17	US-10-666-022-95	Sequence 95, Appl	c 621	3	30.0	33	17	US-10-666-022-164	Sequence 164, App
c 549	3	30.0	29	17	US-10-666-022-120	Sequence 120, App	c 622	3	30.0	33	17	US-10-666-022-164	Sequence 164, App
c 550	3	30.0	29	17	US-10-666-022-120	Sequence 120, App	c 623	3	30.0	33	17	US-10-666-022-174	Sequence 174, App
c 551	3	30.0	29	17	US-10-666-022-130	Sequence 130, App	c 624	3	30.0	33	17	US-10-666-022-174	Sequence 174, App
c 552	3	30.0	29	17	US-10-666-022-130	Sequence 130, App	c 625	3	30.0	33	17	US-10-764-235-35	Sequence 35, Appl
c 553	3	30.0	29	17	US-10-666-022-140	Sequence 140, App	c 626	3	30.0	33	17	US-10-764-235-35	Sequence 35, Appl
c 554	3	30.0	29	17	US-10-666-022-140	Sequence 140, App	c 627	3	30.0	33	17	US-10-758-622-11	GENERAL INFORMA
c 555	3	30.0	29	17	US-10-666-022-150	Sequence 150, App	c 628	3	30.0	33	17	US-10-758-622-11	GENERAL INFORMA
c 556	3	30.0	29	17	US-10-666-022-150	Sequence 150, App	c 629	3	30.0	33	18	US-10-795-667-16	Sequence 16, Appl
c 557	3	30.0	29	17	US-10-666-022-160	Sequence 160, App	c 630	3	30.0	33	18	US-10-795-667-16	Sequence 16, Appl
c 558	3	30.0	29	17	US-10-666-022-160	Sequence 160, App	c 631	3	30.0	34	9	US-09-784-982-13	Sequence 13, Appl
c 559	3	30.0	29	17	US-10-666-022-170	Sequence 170, App	c 632	3	30.0	34	9	US-09-784-982-13	Sequence 13, Appl
c 560	3	30.0	29	17	US-10-666-022-170	Sequence 170, App	c 633	3	30.0	34	15	US-10-211-502-13	Sequence 13, Appl
c 561	3	30.0	29	18	US-10-795-667-12	Sequence 12, Appl	c 634	3	30.0	34	15	US-10-211-502-13	Sequence 13, Appl
c 562	3	30.0	29	18	US-10-795-667-12	Sequence 12, Appl	c 635	3	30.0	34	17	US-10-666-022-175	Sequence 175, App
c 563	3	30.0	30	17	US-10-666-022-76	Sequence 76, Appl	c 636	3	30.0	34	17	US-10-666-022-175	Sequence 175, App
c 564	3	30.0	30	17	US-10-666-022-76	Sequence 76, Appl	c 637	3	30.0	34	18	US-10-795-667-17	Sequence 17, Appl
c 565	3	30.0	30	17	US-10-666-022-86	Sequence 86, Appl	c 638	3	30.0	34	18	US-10-795-667-17	Sequence 17, Appl
c 566	3	30.0	30	17	US-10-666-022-86	Sequence 86, Appl	c 639	3	30.0	35	9	US-09-802-853-9	Sequence 9, Appl
c 567	3	30.0	30	17	US-10-666-022-96	Sequence 96, Appl	c 640	3	30.0	35	9	US-09-802-853-9	Sequence 9, Appl
c 568	3	30.0	30	17	US-10-666-022-96	Sequence 96, Appl	c 641	3	30.0	35	10	US-09-215-163-8	Sequence 8, Appl
c 569	3	30.0	30	17	US-10-666-022-131	Sequence 131, App	c 642	3	30.0	35	10	US-09-215-163-8	Sequence 8, Appl
c 570	3	30.0	30	17	US-10-666-022-131	Sequence 131, App	c 643	3	30.0	35	10	US-09-215-163-8	Sequence 8, Appl
c 571	3	30.0	30	17	US-10-666-022-141	Sequence 141, App	c 644	3	30.0	35	10	US-09-215-163-32	Sequence 32, Appl
c 572	3	30.0	30	17	US-10-666-022-141	Sequence 141, App	c 645	3	30.0	35	10	US-09-215-163-32	Sequence 32, Appl
c 573	3	30.0	30	17	US-10-666-022-151	Sequence 151, App	c 646	3	30.0	35	14	US-10-307-385-9	Sequence 9, Appl
c 574	3	30.0	30	17	US-10-666-022-151	Sequence 151, App	c 647	3	30.0	35	14	US-10-307-385-9	Sequence 9, Appl
c 575	3	30.0	30	17	US-10-666-022-151	Sequence 151, App	c 648	3	30.0	35	15	US-10-280-261-6	Sequence 6, Appl
c 576	3	30.0	30	17	US-10-666-022-161	Sequence 161, App	c 649	3	30.0	35	15	US-10-280-261-6	Sequence 6, Appl
c 577	3	30.0	30	17	US-10-666-022-161	Sequence 161, App	c 650	3	30.0	36	9	US-09-753-436-40	Sequence 40, Appl
c 578	3	30.0	30	17	US-10-666-022-171	Sequence 171, App	c 651	3	30.0	36	15	US-10-126-845-35	Sequence 35, Appl
c 579	3	30.0	30	17	US-10-666-022-171	Sequence 171, App	c 652	3	30.0	36	15	US-10-126-845-35	Sequence 35, Appl
c 580	3	30.0	30	17	US-10-764-235-36	Sequence 36, Appl	c 653	3	30.0	36	15	US-10-126-845-35	Sequence 35, Appl
c 581	3	30.0	30	17	US-10-764-235-36	Sequence 36, Appl	c 654	3	30.0	36	15	US-10-163-942-40	Sequence 40, Appl
c 582	3	30.0	30	18	US-10-795-667-13	Sequence 13, Appl	c 655	3	30.0	36	15	US-10-163-942-40	Sequence 40, Appl
c 583	3	30.0	30	18	US-10-795-667-19	Sequence 19, Appl	c 656	3	30.0	36	15	US-10-418-182-87	Sequence 87, Appl
c 584	3	30.0	30	18	US-10-795-667-19	Sequence 19, Appl	c 657	3	30.0	36	15	US-10-418-182-87	Sequence 87, Appl
c 585	3	30.0	30	18	US-10-795-667-20	Sequence 20, Appl	c 658	3	30.0	36	15	US-10-418-182-400	Sequence 400, App
c 586	3	30.0	30	18	US-10-795-667-20	Sequence 20, Appl	c 659	3	30.0	36	15	US-10-418-182-400	Sequence 400, App
c 587	3	30.0	31	16	US-10-333-578-8	Sequence 8, Appl	c 660	3	30.0	36	18	US-10-745-115-40	Sequence 40, Appl
c 588	3	30.0	31	16	US-10-333-578-8	Sequence 8, Appl	c 661	3	30.0	36	18	US-10-745-115-40	Sequence 40, Appl
c 589	3	30.0	31	17	US-10-666-022-87	Sequence 87, Appl	c 662	3	30.0	38	15	US-10-209-507-13	Sequence 13, Appl
c 590	3	30.0	31	17	US-10-666-022-87	Sequence 87, Appl	c 663	3	30.0	38	15	US-10-209-507-13	Sequence 13, Appl
c 591	3	30.0	31	17	US-10-666-022-97	Sequence 97, Appl	c 664	3	30.0	38	15	US-10-280-261-15	Sequence 15, Appl
c 592	3	30.0	31	17	US-10-666-022-97	Sequence 97, Appl	c 665	3	30.0	38	15	US-10-280-261-15	Sequence 15, Appl
c 593	3	30.0	31	17	US-10-666-022-142	Sequence 142, App	c 666	3	30.0	38	17	US-10-302-570-8	Sequence 8, Appl
c 594	3	30.0	31	17	US-10-666-022-142	Sequence 142, App	c 667	3	30.0	39	9	US-09-564-329A-26	Sequence 26, Appl
c 595	3	30.0	31	17	US-10-666-022-152	Sequence 152, App	c 668	3	30.0	39	9	US-09-564-329A-26	Sequence 26, Appl
c 596	3	30.0	31	17	US-10-666-022-152	Sequence 152, App	c 669	3	30.0	39	9	US-09-881-823-26	Sequence 26, Appl

c 670	3	30.0	39	9	US-09-881-823-26	Sequence 26, Appl	743	3	30.0	51	15	US-10-418-182-314	Sequence 314, App
c 671	3	30.0	39	9	US-09-855-153-26	Sequence 26, Appl	c 744	3	30.0	51	15	US-10-418-182-314	Sequence 314, App
c 672	3	30.0	39	9	US-09-855-153-26	Sequence 26, Appl	745	3	30.0	51	15	US-10-418-182-326	Sequence 326, App
c 673	3	30.0	39	9	US-09-854-811-26	Sequence 26, Appl	c 746	3	30.0	51	15	US-10-418-182-326	Sequence 326, App
c 674	3	30.0	39	9	US-09-854-811-26	Sequence 26, Appl	747	3	30.0	51	15	US-10-418-182-338	Sequence 338, App
c 675	3	30.0	39	9	US-09-934-773-26	Sequence 26, Appl	c 748	3	30.0	51	15	US-10-418-182-338	Sequence 338, App
c 676	3	30.0	39	9	US-09-934-773-26	Sequence 26, Appl	749	3	30.0	51	15	US-10-418-182-362	Sequence 362, App
c 677	3	30.0	39	9	US-09-963-620-26	Sequence 26, Appl	c 750	3	30.0	51	15	US-10-418-182-362	Sequence 362, App
c 678	3	30.0	39	9	US-09-963-620-26	Sequence 26, Appl	751	3	30.0	51	15	US-10-418-182-398	Sequence 398, App
c 679	3	30.0	39	10	US-09-855-632-26	Sequence 26, Appl	c 752	3	30.0	51	15	US-10-418-182-398	Sequence 398, App
c 680	3	30.0	39	10	US-09-855-632-26	Sequence 26, Appl	753	3	30.0	54	15	US-10-418-182-267	Sequence 267, App
c 681	3	30.0	39	14	US-10-121-258-59	Sequence 59, Appl	c 754	3	30.0	54	15	US-10-418-182-267	Sequence 267, App
c 682	3	30.0	39	14	US-10-121-258-59	Sequence 59, Appl	755	3	30.0	54	15	US-10-418-182-273	Sequence 273, App
c 683	3	30.0	39	15	US-10-325-784-26	Sequence 26, Appl	c 756	3	30.0	54	15	US-10-418-182-273	Sequence 273, App
c 684	3	30.0	39	15	US-10-325-784-26	Sequence 26, Appl	757	3	30.0	54	15	US-10-418-182-275	Sequence 275, App
c 685	3	30.0	39	15	US-10-224-720-26	Sequence 26, Appl	c 758	3	30.0	54	15	US-10-418-182-275	Sequence 275, App
c 686	3	30.0	39	15	US-10-224-720-26	Sequence 26, Appl	759	3	30.0	54	15	US-10-418-182-277	Sequence 277, App
c 687	3	30.0	39	15	US-10-225-779-26	Sequence 26, Appl	c 760	3	30.0	54	15	US-10-418-182-277	Sequence 277, App
c 688	3	30.0	39	15	US-10-225-779-26	Sequence 26, Appl	761	3	30.0	54	15	US-10-418-182-283	Sequence 283, App
c 689	3	30.0	39	15	US-10-374-381-26	Sequence 26, Appl	c 762	3	30.0	54	15	US-10-418-182-283	Sequence 283, App
c 690	3	30.0	39	15	US-10-374-381-26	Sequence 26, Appl	763	3	30.0	54	15	US-10-418-182-315	Sequence 315, App
c 691	3	30.0	39	16	US-10-446-542-26	Sequence 26, Appl	c 764	3	30.0	54	15	US-10-418-182-315	Sequence 315, App
c 692	3	30.0	39	16	US-10-446-542-26	Sequence 26, Appl	765	3	30.0	54	15	US-10-418-182-333	Sequence 333, App
c 693	3	30.0	39	18	US-10-446-542-26	Sequence 26, Appl	c 766	3	30.0	54	15	US-10-418-182-333	Sequence 333, App
c 694	3	30.0	39	18	US-10-769-308-20	Sequence 20, Appl	767	3	30.0	54	15	US-10-418-182-339	Sequence 339, App
c 695	3	30.0	39	18	US-10-769-308-20	Sequence 20, Appl	c 768	3	30.0	54	15	US-10-418-182-339	Sequence 339, App
c 696	3	30.0	40	17	US-10-693-057-441	Sequence 441, App	769	3	30.0	54	15	US-10-418-182-345	Sequence 345, App
c 697	3	30.0	40	17	US-10-693-057-441	Sequence 441, App	c 770	3	30.0	54	15	US-10-418-182-345	Sequence 345, App
c 698	3	30.0	40	17	US-10-693-057-443	Sequence 443, App	771	3	30.0	54	15	US-10-418-182-363	Sequence 363, App
c 699	3	30.0	40	17	US-10-693-057-443	Sequence 443, App	c 772	3	30.0	54	15	US-10-418-182-363	Sequence 363, App
c 700	3	30.0	40	17	US-10-693-057-444	Sequence 444, App	773	3	30.0	56	17	US-10-693-057-448	Sequence 448, App
c 701	3	30.0	40	17	US-10-693-057-444	Sequence 444, App	c 774	3	30.0	56	17	US-10-693-057-448	Sequence 448, App
c 702	3	30.0	40	17	US-10-693-057-446	Sequence 446, App	775	3	30.0	56	17	US-10-693-057-459	Sequence 459, App
c 703	3	30.0	40	17	US-10-693-057-446	Sequence 446, App	c 776	3	30.0	56	17	US-10-693-057-459	Sequence 459, App
c 704	3	30.0	40	17	US-10-693-057-482	Sequence 482, App	777	3	30.0	56	17	US-10-693-057-489	Sequence 489, App
c 705	3	30.0	40	17	US-10-693-057-482	Sequence 482, App	c 778	3	30.0	56	17	US-10-693-057-489	Sequence 489, App
c 706	3	30.0	40	17	US-10-693-057-484	Sequence 484, App	779	3	30.0	56	17	US-10-693-057-500	Sequence 500, App
c 707	3	30.0	40	17	US-10-693-057-484	Sequence 484, App	c 780	3	30.0	56	17	US-10-693-057-500	Sequence 500, App
c 708	3	30.0	40	17	US-10-693-057-485	Sequence 485, App	781	3	30.0	59	9	US-09-796-071-14	Sequence 14, Appl
c 709	3	30.0	40	17	US-10-693-057-485	Sequence 485, App	c 782	3	30.0	59	9	US-09-796-071-14	Sequence 14, Appl
c 710	3	30.0	40	17	US-10-693-057-487	Sequence 487, App	783	3	30.0	59	17	US-10-616-228-14	Sequence 14, Appl
c 711	3	30.0	40	17	US-10-693-057-487	Sequence 487, App	c 784	3	30.0	59	17	US-10-616-228-14	Sequence 14, Appl
c 712	3	30.0	41	16	US-10-035-833A-5145	Sequence 5145, App	785	3	30.0	60	18	US-10-149-835C-5	Sequence 5, Appl1
c 713	3	30.0	41	16	US-10-035-833A-5145	Sequence 5145, App	c 786	3	30.0	60	18	US-10-149-835C-5	Sequence 5, Appl1
c 714	3	30.0	41	16	US-10-035-833A-5146	Sequence 5146, App	787	3	30.0	60	18	US-10-149-835C-6	Sequence 6, Appl1
c 715	3	30.0	42	8	US-08-934-000-23	Sequence 23, Appl	c 788	3	30.0	60	18	US-10-149-835C-6	Sequence 6, Appl1
c 716	3	30.0	42	8	US-08-934-000-23	Sequence 23, Appl	789	3	30.0	61	10	US-09-849-928-377	Sequence 377, App
c 717	3	30.0	42	10	US-09-977-283A-23	Sequence 23, Appl	c 790	3	30.0	61	10	US-09-849-928-377	Sequence 377, App
c 718	3	30.0	42	10	US-09-977-283A-23	Sequence 23, Appl	791	3	30.0	61	14	US-10-066-960-377	Sequence 377, App
c 719	3	30.0	45	15	US-10-205-911-6	Sequence 6, Appl1	c 792	3	30.0	61	14	US-10-066-960-377	Sequence 377, App
c 720	3	30.0	45	15	US-10-205-911-6	Sequence 6, Appl1	793	3	30.0	61	16	US-10-409-627-377	Sequence 377, App
c 721	3	30.0	45	15	US-10-205-911-7	Sequence 7, Appl1	c 794	3	30.0	61	16	US-10-409-627-377	Sequence 377, App
c 722	3	30.0	45	15	US-10-205-911-7	Sequence 7, Appl1	795	3	30.0	61	16	US-10-705-300-377	Sequence 377, App
c 723	3	30.0	45	15	US-10-205-911-11	Sequence 11, Appl	c 796	3	30.0	61	16	US-10-705-300-377	Sequence 377, App
c 724	3	30.0	45	15	US-10-205-911-11	Sequence 11, Appl	797	3	30.0	62	17	US-10-693-057-460	Sequence 460, App
c 725	3	30.0	45	15	US-10-205-911-11	Sequence 11, Appl	c 798	3	30.0	62	17	US-10-693-057-460	Sequence 460, App
c 726	3	30.0	47	16	US-10-349-143-3789	Sequence 3789, App	799	3	30.0	62	17	US-10-693-057-501	Sequence 501, App
c 727	3	30.0	48	15	US-10-349-143-3789	Sequence 3789, App	c 800	3	30.0	62	17	US-10-693-057-501	Sequence 501, App
c 728	3	30.0	48	15	US-10-394-192-8	Sequence 8, Appl1	801	3	30.0	65	17	US-10-693-057-449	Sequence 449, App
c 729	3	30.0	50	17	US-10-693-057-447	Sequence 447, App	c 802	3	30.0	65	17	US-10-693-057-449	Sequence 449, App
c 730	3	30.0	50	17	US-10-693-057-447	Sequence 447, App	803	3	30.0	65	17	US-10-693-057-490	Sequence 490, App
c 731	3	30.0	50	17	US-10-693-057-488	Sequence 488, App	c 804	3	30.0	65	17	US-10-693-057-490	Sequence 490, App
c 732	3	30.0	50	17	US-10-693-057-488	Sequence 488, App	805	3	30.0	66	9	US-09-933-797-469	Sequence 469, App
c 733	3	30.0	51	15	US-10-418-182-225	Sequence 225, App	c 806	3	30.0	66	9	US-09-933-797-469	Sequence 469, App
c 734	3	30.0	51	15	US-10-418-182-225	Sequence 225, App	807	3	30.0	67	14	US-10-184-644-248	Sequence 248, App
c 735	3	30.0	51	15	US-10-418-182-229	Sequence 229, App	c 808	3	30.0	67	14	US-10-184-644-248	Sequence 248, App
c 736	3	30.0	51	15	US-10-418-182-229	Sequence 229, App	809	3	30.0	67	14	US-10-184-634-248	Sequence 248, App
c 737	3	30.0	51	15	US-10-418-182-233	Sequence 233, App	c 810	3	30.0	67	14	US-10-184-634-248	Sequence 248, App
c 738	3	30.0	51	15	US-10-418-182-233	Sequence 233, App	811	3	30.0	70	10	US-09-849-928-369	Sequence 369, App
c 739	3	30.0	51	15	US-10-418-182-241	Sequence 241, App	c 812	3	30.0	70	10	US-09-849-928-369	Sequence 369, App
c 740	3	30.0	51	15	US-10-418-182-241	Sequence 241, App	813	3	30.0	70	14	US-10-066-960-369	Sequence 369, App
c 741	3	30.0	51	15	US-10-418-182-253	Sequence 253, App	c 814	3	30.0	70	14	US-10-066-960-369	Sequence 369, App
c 742	3	30.0	51	15	US-10-418-182-253	Sequence 253, App	815	3	30.0	70	16	US-10-409-627-369	Sequence 369, App

c 816	3	30.0	70	16	US-10-409-627-369	Sequence 369, App	889	3	30.0	84	17	US-10-693-057-379	Sequence 379, App
c 817	3	30.0	70	16	US-10-705-300-369	Sequence 369, App	c 890	3	30.0	84	17	US-10-693-057-379	Sequence 379, App
c 818	3	30.0	70	16	US-10-705-300-369	Sequence 369, App	c 891	3	30.0	84	17	US-10-693-057-380	Sequence 380, App
c 819	3	30.0	71	10	US-09-849-928-382	Sequence 382, App	c 892	3	30.0	84	17	US-10-693-057-380	Sequence 380, App
c 820	3	30.0	71	10	US-09-849-928-382	Sequence 382, App	c 893	3	30.0	84	18	US-10-333-872A-213	Sequence 213, App
c 821	3	30.0	71	14	US-10-066-960-382	Sequence 382, App	c 894	3	30.0	84	18	US-10-333-872A-213	Sequence 213, App
c 822	3	30.0	71	14	US-10-066-960-382	Sequence 382, App	c 895	3	30.0	85	15	US-10-400-053-6	Sequence 6, Appli
c 823	3	30.0	71	16	US-10-409-627-382	Sequence 382, App	c 896	3	30.0	85	15	US-10-400-053-6	Sequence 6, Appli
c 824	3	30.0	71	16	US-10-409-627-382	Sequence 382, App	c 897	3	30.0	89	14	US-10-184-644-566	Sequence 566, App
c 825	3	30.0	71	16	US-10-705-300-382	Sequence 382, App	c 898	3	30.0	89	14	US-10-184-644-566	Sequence 566, App
c 826	3	30.0	71	16	US-10-705-300-382	Sequence 382, App	c 899	3	30.0	89	14	US-10-184-634-566	Sequence 566, App
c 827	3	30.0	71	17	US-10-693-057-450	Sequence 450, App	c 900	3	30.0	89	14	US-10-184-634-566	Sequence 566, App
c 828	3	30.0	71	17	US-10-693-057-450	Sequence 450, App	c 901	3	30.0	89	17	US-10-693-057-464	Sequence 464, App
c 829	3	30.0	71	17	US-10-693-057-461	Sequence 461, App	c 902	3	30.0	89	17	US-10-693-057-464	Sequence 464, App
c 830	3	30.0	71	17	US-10-693-057-461	Sequence 461, App	c 903	3	30.0	89	17	US-10-693-057-505	Sequence 505, App
c 831	3	30.0	71	17	US-10-693-057-491	Sequence 491, App	c 904	3	30.0	89	17	US-10-693-057-505	Sequence 505, App
c 832	3	30.0	71	17	US-10-693-057-491	Sequence 491, App	c 905	3	30.0	90	16	US-10-296-734-108	Sequence 108, App
c 833	3	30.0	71	17	US-10-693-057-502	Sequence 502, App	c 906	3	30.0	90	16	US-10-296-734-108	Sequence 108, App
c 834	3	30.0	71	17	US-10-693-057-502	Sequence 502, App	c 907	3	30.0	90	16	US-10-296-734-110	Sequence 110, App
c 835	3	30.0	72	18	US-10-311-976A-15	Sequence 15, Appl	c 908	3	30.0	90	16	US-10-296-734-110	Sequence 110, App
c 836	3	30.0	72	18	US-10-311-976A-15	Sequence 15, Appl	c 909	3	30.0	90	16	US-10-296-734-188	Sequence 188, App
c 837	3	30.0	72	18	US-10-311-976A-16	Sequence 16, Appl	c 910	3	30.0	90	16	US-10-296-734-188	Sequence 188, App
c 838	3	30.0	72	18	US-10-311-976A-16	Sequence 16, Appl	c 911	3	30.0	90	16	US-10-296-734-234	Sequence 234, App
c 839	3	30.0	77	17	US-10-693-057-451	Sequence 451, App	c 912	3	30.0	90	16	US-10-296-734-234	Sequence 234, App
c 840	3	30.0	77	17	US-10-693-057-451	Sequence 451, App	c 913	3	30.0	90	16	US-10-296-734-236	Sequence 236, App
c 841	3	30.0	77	17	US-10-693-057-462	Sequence 462, App	c 914	3	30.0	90	16	US-10-296-734-236	Sequence 236, App
c 842	3	30.0	77	17	US-10-693-057-462	Sequence 462, App	c 915	3	30.0	90	16	US-10-296-734-256	Sequence 256, App
c 843	3	30.0	77	17	US-10-693-057-492	Sequence 492, App	c 916	3	30.0	90	16	US-10-296-734-256	Sequence 256, App
c 844	3	30.0	77	17	US-10-693-057-492	Sequence 492, App	c 917	3	30.0	91	13	US-10-092-140-5	Sequence 5, Appli
c 845	3	30.0	77	17	US-10-693-057-503	Sequence 503, App	c 918	3	30.0	91	13	US-10-092-140-5	Sequence 5, Appli
c 846	3	30.0	77	17	US-10-693-057-503	Sequence 503, App	c 919	3	30.0	95	14	US-10-123-155-62	Sequence 62, Appl
c 847	3	30.0	79	17	US-10-693-057-440	Sequence 440, App	c 920	3	30.0	95	14	US-10-123-155-62	Sequence 62, Appl
c 848	3	30.0	79	17	US-10-693-057-440	Sequence 440, App	c 921	3	30.0	95	15	US-10-146-731-62	Sequence 62, Appl
c 849	3	30.0	79	17	US-10-693-057-481	Sequence 481, App	c 922	3	30.0	95	15	US-10-146-731-62	Sequence 62, Appl
c 850	3	30.0	79	17	US-10-693-057-481	Sequence 481, App	c 923	3	30.0	95	15	US-10-140-472-62	Sequence 62, Appl
c 851	3	30.0	81	14	US-10-112-612-34	Sequence 34, Appl	c 924	3	30.0	95	15	US-10-140-472-62	Sequence 62, Appl
c 852	3	30.0	81	14	US-10-112-612-34	Sequence 34, Appl	c 925	3	30.0	95	15	US-10-141-761-62	Sequence 62, Appl
c 853	3	30.0	81	15	US-10-112-691-34	Sequence 34, Appl	c 926	3	30.0	95	15	US-10-141-761-62	Sequence 62, Appl
c 854	3	30.0	81	15	US-10-112-691-34	Sequence 34, Appl	c 927	3	30.0	95	15	US-10-142-885-62	Sequence 62, Appl
c 855	3	30.0	81	15	US-10-423-495-36	Sequence 36, Appl	c 928	3	30.0	95	15	US-10-142-885-62	Sequence 62, Appl
c 856	3	30.0	81	15	US-10-423-495-36	Sequence 36, Appl	c 929	3	30.0	95	15	US-10-158-790-62	Sequence 62, Appl
c 857	3	30.0	82	17	US-10-693-057-439	Sequence 439, App	c 930	3	30.0	95	15	US-10-158-790-62	Sequence 62, Appl
c 858	3	30.0	82	17	US-10-693-057-439	Sequence 439, App	c 931	3	30.0	95	15	US-10-137-871-62	Sequence 62, Appl
c 859	3	30.0	82	17	US-10-693-057-480	Sequence 480, App	c 932	3	30.0	95	15	US-10-137-871-62	Sequence 62, Appl
c 860	3	30.0	82	17	US-10-693-057-480	Sequence 480, App	c 933	3	30.0	95	15	US-10-140-923-62	Sequence 62, Appl
c 861	3	30.0	83	17	US-10-693-057-452	Sequence 452, App	c 934	3	30.0	95	15	US-10-140-923-62	Sequence 62, Appl
c 862	3	30.0	83	17	US-10-693-057-452	Sequence 452, App	c 935	3	30.0	95	15	US-10-141-756-62	Sequence 62, Appl
c 863	3	30.0	83	17	US-10-693-057-463	Sequence 463, App	c 936	3	30.0	95	15	US-10-141-756-62	Sequence 62, Appl
c 864	3	30.0	83	17	US-10-693-057-493	Sequence 493, App	c 937	3	30.0	95	15	US-10-141-759-62	Sequence 62, Appl
c 865	3	30.0	83	17	US-10-693-057-493	Sequence 493, App	c 938	3	30.0	95	15	US-10-141-759-62	Sequence 62, Appl
c 866	3	30.0	83	17	US-10-693-057-493	Sequence 493, App	c 939	3	30.0	95	15	US-10-140-805-62	Sequence 62, Appl
c 867	3	30.0	83	17	US-10-693-057-504	Sequence 504, App	c 940	3	30.0	95	15	US-10-140-805-62	Sequence 62, Appl
c 868	3	30.0	84	14	US-10-184-644-186	Sequence 186, App	c 941	3	30.0	95	15	US-10-140-864-62	Sequence 62, Appl
c 869	3	30.0	84	14	US-10-184-644-186	Sequence 186, App	c 942	3	30.0	95	15	US-10-140-864-62	Sequence 62, Appl
c 870	3	30.0	84	14	US-10-112-612-61	Sequence 61, Appl	c 943	3	30.0	95	16	US-10-142-426-62	Sequence 62, Appl
c 871	3	30.0	84	14	US-10-112-612-61	Sequence 61, Appl	c 944	3	30.0	95	16	US-10-142-426-62	Sequence 62, Appl
c 872	3	30.0	84	14	US-10-184-644-186	Sequence 186, App	c 945	3	30.0	97	10	US-09-849-928-272	Sequence 272, App
c 873	3	30.0	84	14	US-10-184-644-186	Sequence 186, App	c 946	3	30.0	97	10	US-09-849-928-272	Sequence 272, App
c 874	3	30.0	84	14	US-10-184-634-186	Sequence 186, App	c 947	3	30.0	97	14	US-10-066-960-272	Sequence 272, App
c 875	3	30.0	84	14	US-10-133-128-229	Sequence 229, App	c 948	3	30.0	97	14	US-10-066-960-272	Sequence 272, App
c 876	3	30.0	84	14	US-10-133-128-229	Sequence 229, App	c 949	3	30.0	97	16	US-10-409-627-272	Sequence 272, App
c 877	3	30.0	84	14	US-10-133-128-230	Sequence 230, App	c 950	3	30.0	97	16	US-10-409-627-272	Sequence 272, App
c 878	3	30.0	84	15	US-10-133-128-230	Sequence 230, App	c 951	3	30.0	97	16	US-10-705-300-272	Sequence 272, App
c 879	3	30.0	84	15	US-10-289-660-229	Sequence 229, App	c 952	3	30.0	97	16	US-10-705-300-272	Sequence 272, App
c 880	3	30.0	84	15	US-10-289-660-229	Sequence 229, App	c 953	3	30.0	100	14	US-10-184-644-526	Sequence 526, App
c 881	3	30.0	84	15	US-10-289-660-230	Sequence 230, App	c 954	3	30.0	100	14	US-10-184-644-526	Sequence 526, App
c 882	3	30.0	84	15	US-10-289-660-230	Sequence 230, App	c 955	3	30.0	100	14	US-10-184-634-526	Sequence 526, App
c 883	3	30.0	84	15	US-10-112-691-61	Sequence 61, Appl	c 956	3	30.0	100	14	US-10-184-634-526	Sequence 526, App
c 884	3	30.0	84	15	US-10-112-691-61	Sequence 61, Appl	c 957	2	20.0	4	9	US-09-760-506-5	Sequence 5, Appli
c 885	3	30.0	84	15	US-10-063-685-44	Sequence 44, Appl	c 958	2	20.0	4	9	US-09-760-506-5	Sequence 5, Appli
c 886	3	30.0	84	15	US-10-063-685-44	Sequence 44, Appl	c 959	2	20.0	4	17	US-10-293-252C-2	Sequence 2, Appli
c 887	3	30.0	84	15	US-10-423-495-58	Sequence 58, Appl	c 960	2	20.0	4	17	US-10-293-252C-2	Sequence 2, Appli
c 888	3	30.0	84	15	US-10-423-495-58	Sequence 58, Appl	c 961	2	20.0	4	17	US-10-293-252C-6	Sequence 6, Appli



;  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-813-824A-3

Query Match 100.0%; Score 10; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
|||  
Db 10 RRRCWGYYY 1

RESULT 3  
US-09-928-385B-24  
; Sequence 24, Application US/09928385B  
; Publication No. US20030049625A1  
; GENERAL INFORMATION:  
; APPLICANT: Heyduk, Tomasz  
; TITLE OF INVENTION: A Rapid and Sensitive Proximity-Based Assay for the Detection  
; FILE REFERENCE: 16153-7963  
; CURRENT APPLICATION NUMBER: US/09/928,385B  
; CURRENT FILING DATE: 2002-01-14  
; NUMBER OF SEQ ID NOS: 24  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: These sequences were chemically synthesized,  
; OTHER INFORMATION: but may also be created via recombinant methods.  
US-09-928-385B-24

Query Match 100.0%; Score 10; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
|||  
Db 1 RRRCWGYYY 10

RESULT 4  
US-09-928-385B-24/c  
; Sequence 24, Application US/09928385B  
; Publication No. US20030049625A1  
; GENERAL INFORMATION:  
; APPLICANT: Heyduk, Tomasz  
; TITLE OF INVENTION: A Rapid and Sensitive Proximity-Based Assay for the Detection  
; FILE REFERENCE: 16153-7963  
; CURRENT APPLICATION NUMBER: US/09/928,385B  
; CURRENT FILING DATE: 2002-01-14  
; NUMBER OF SEQ ID NOS: 24  
; SEQ ID NO 24  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: These sequences were chemically synthesized,  
; OTHER INFORMATION: but may also be created via recombinant methods.  
US-09-928-385B-24

Query Match 100.0%; Score 10; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
|||  
Db 10 RRRCWGYYY 1

RESULT 5  
US-09-798-883B-57  
; Sequence 57, Application US/09798883B  
; Publication No. US20030159159A1  
; GENERAL INFORMATION:  
; APPLICANT: LINNIK, Matthew  
; APPLICANT: RACKE, Margaret  
; APPLICANT: KRAKOWSKY, Joan  
; APPLICANT: SUBRAMANIAM, Arun  
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and Exon 3 Promoters  
; FILE REFERENCE: HMR2002C US DIV  
; CURRENT APPLICATION NUMBER: US/09/798,883B  
; CURRENT FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 57  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Consensus Binding Motif in Human Nerve Growth Factor Exon 1 and Exon 3  
; OTHER INFORMATION: Promoter  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: r=g or a  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: w=a or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: y=c or t  
US-09-798-883B-57

Query Match 100.0%; Score 10; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
|||  
Db 1 RRRCWGYYY 10

RESULT 6  
US-09-798-883B-57/c  
; Sequence 57, Application US/09798883B  
; Publication No. US20030159159A1  
; GENERAL INFORMATION:  
; APPLICANT: LINNIK, Matthew  
; APPLICANT: RACKE, Margaret  
; APPLICANT: KRAKOWSKY, Joan  
; APPLICANT: SUBRAMANIAM, Arun  
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and Exon 3 Promoters  
; FILE REFERENCE: HMR2002C US DIV  
; CURRENT APPLICATION NUMBER: US/09/798,883B  
; CURRENT FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 57  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Consensus Binding Motif in Human Nerve Growth Factor Exon 1 and Exon 3  
; OTHER INFORMATION: Promoter  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: r=g or a  
; FEATURE:  
US-09-798-883B-57

Query Match 100.0%; Score 10; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NAME/KEY: misc feature  
 OTHER INFORMATION: w=a or t  
 FEATURE:  
 NAME/KEY: misc feature  
 OTHER INFORMATION: y=c or t  
 US-09-798-883B-57

Query Match 100.0%; Score 10; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
 |||||  
 Db 10 RRRCWGYYY 1

## RESULT 7

US-09-326-885-57  
 ; Sequence 57, Application US/09326885  
 ; Publication No. US20030192065A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Linnik, Matthew D  
 ; Racke, Margaret M  
 ; Krakowsky, Joan M  
 ; Subramaniam, Arun  
 ; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and  
 ; Exon 3 Promoters

NUMBER OF SEQUENCES: 84  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hoechst Marion Roussel, Inc.  
 ; STREET: 2110 East Galbraith Road, P.O. Box 156300  
 ; CITY: Cincinnati  
 ; STATE: Ohio  
 ; COUNTRY: United States of America  
 ; ZIP: 45215-6300

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/326,885  
 ; FILING DATE: 07-Jun-1999  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/020,179  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: US 60/038,212  
 ; FILING DATE: 06-FEB-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Payne, T. Helen  
 ; REGISTRATION NUMBER: 36,889  
 ; REFERENCE/DOCKET NUMBER: HMR2002A  
 ; TELEPHONE: 513 948-7183  
 ; TELEFAX: 513 948-7961/4681  
 ; TELEX: 214320

INFORMATION FOR SEQ ID NO: 57:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: DNA (genomic)  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
 US-09-326-885-57

Query Match 100.0%; Score 10; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
 |||||  
 Db 10 RRRCWGYYY 1

NAME/KEY: misc feature  
 OTHER INFORMATION: w=a or t  
 FEATURE:  
 NAME/KEY: misc feature  
 OTHER INFORMATION: y=c or t  
 US-09-798-883B-57

Query Match 100.0%; Score 10; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
 |||||  
 Db 10 RRRCWGYYY 1

## RESULT 8

US-09-326-885-57/c  
 ; Sequence 57, Application US/09326885  
 ; Publication No. US20030192065A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Linnik, Matthew D  
 ; Racke, Margaret M  
 ; Krakowsky, Joan M  
 ; Subramaniam, Arun  
 ; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and  
 ; Exon 3 Promoters

NUMBER OF SEQUENCES: 84  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hoechst Marion Roussel, Inc.  
 ; STREET: 2110 East Galbraith Road, P.O. Box 156300  
 ; CITY: Cincinnati  
 ; STATE: Ohio  
 ; COUNTRY: United States of America  
 ; ZIP: 45215-6300

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/326,885  
 ; FILING DATE: 07-Jun-1999  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/020,179  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: US 60/038,212  
 ; FILING DATE: 06-FEB-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Payne, T. Helen  
 ; REGISTRATION NUMBER: 36,889  
 ; REFERENCE/DOCKET NUMBER: HMR2002A  
 ; TELEPHONE: 513 948-7183  
 ; TELEFAX: 513 948-7961/4681  
 ; TELEX: 214320

INFORMATION FOR SEQ ID NO: 57:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: DNA (genomic)  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
 US-09-326-885-57

Query Match 100.0%; Score 10; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
 |||||  
 Db 10 RRRCWGYYY 1

## RESULT 9

US-10-464-996-5  
 ; Sequence 5, Application US/10464996  
 ; Publication No. US20040101915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Devereaux, Quinn L.  
 ; APPLICANT: Wagner, Klaus W.  
 ; APPLICANT: Hampton, Garret M.  
 ; APPLICANT: IRM LLC  
 ; TITLE OF INVENTION: Diagnosis and Treatment of Chemoresistant Tumors

```
; FILE REFERENCE: 021288-001220US
; CURRENT APPLICATION NUMBER: US/10/464,996
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/390,256
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/456,585
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:p53 consensus
; OTHER INFORMATION: element
US-10-464-996-5

Query Match      100.0%; Score 10; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 1 RRRRCWGGYY 10

RESULT 10
US-10-464-996-5/c
; Sequence 5, Application US/10464996
; Publication No. US20040101915A1
; GENERAL INFORMATION:
; APPLICANT: Deveraux, Quinn L.
; APPLICANT: Wagner, Klaus W.
; APPLICANT: Hampton, Garret M.
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Diagnosis and Treatment of Chemoresistant Tumors
; FILE REFERENCE: 021288-001220US
; CURRENT APPLICATION NUMBER: US/10/464,996
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/390,256
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/456,585
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:p53 consensus
; OTHER INFORMATION: element
US-10-464-996-5

Query Match      100.0%; Score 10; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 10 RRRRCWGGYY 1

RESULT 11
US-10-795-933-21
; Sequence 21, Application US/10795933
; Publication No. US20040259126A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
```

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; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/10/795,933
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/08/260,190
; PRIOR FILING DATE: 1994-06-15
; PRIOR APPLICATION NUMBER: 08/177,093
; PRIOR FILING DATE: 1993-12-30
; PRIOR APPLICATION NUMBER: 07/964,589
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: PV-709-92
; PRIOR FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(10)
US-10-795-933-21

Query Match      100.0%; Score 10; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 1 RRRRCWGGYY 10

RESULT 12
US-10-795-933-21/c
; Sequence 21, Application US/10795933
; Publication No. US20040259126A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/10/795,933
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/08/260,190
; PRIOR FILING DATE: 1994-06-15
; PRIOR APPLICATION NUMBER: 08/177,093
; PRIOR FILING DATE: 1993-12-30
; PRIOR APPLICATION NUMBER: 07/964,589
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: PV-709-92
; PRIOR FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(10)
US-10-795-933-21

Query Match      100.0%; Score 10; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 10 RRRRCWGGYY 1

RESULT 13
US-10-450-436-26
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; Sequence 26, Application US/10450436
; Publication No. US20040077832A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jian
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: JFV1 induces rapid apoptosis
; FILE REFERENCE: 01107.00062
; CURRENT APPLICATION NUMBER: US/10/450.436
; CURRENT FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-436-26

Query Match      100.0%; Score 10; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRCWGWGYYY 10
Db      |||||
        10 RRCWGWGYYY 19

RESULT 14
US-10-450-436-26/c
; Sequence 26, Application US/10450436
; Publication No. US20040077832A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jian
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: JFV1 induces rapid apoptosis
; FILE REFERENCE: 01107.00062
; CURRENT APPLICATION NUMBER: US/10/450.436
; CURRENT FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-436-26

Query Match      100.0%; Score 10; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRCWGWGYYY 10
Db      |||||
        10 RRCWGWGYYY 19

RESULT 15
US-09-939-581A-6
; Sequence 6, Application US/09939581A
; Patent No. US20020102245A1
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; CURRENT APPLICATION NUMBER: US/09/939,581A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/210,748
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-939-581A-6

Query Match      100.0%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRCWGWGYYY 10
Db      |||||
        20 RRCWGWGYYY 11

RESULT 16
US-09-939-581A-6/c
; Sequence 6, Application US/09939581A
; Patent No. US20020102245A1
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; CURRENT APPLICATION NUMBER: US/09/939,581A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/210,748
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-939-581A-6

Query Match      100.0%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRCWGWGYYY 10
Db      |||||
        20 RRCWGWGYYY 11

RESULT 17
US-09-816-763-92
; Sequence 92, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor P53
US-09-816-763-92

Query Match      100.0%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10  
|||||  
Db 1 RRRCWGYYY 10

RESULT 18  
US-10-816-763-92/c  
; Sequence 92, Application US/09816763  
; Patent No. US20020110814A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING. THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001AUS  
; CURRENT APPLICATION NUMBER: US/09/816,763  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 92  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence for transcriptional factor P53  
US-09-816-763-92

Query Match 100.0%; Score 10; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10  
|||||  
Db 20 RRRCWGYYY 11

RESULT 19  
US-10-821-568-92  
; Sequence 92, Application US/10821568  
; Publication No. US20040185497A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING. THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001DV1  
; CURRENT APPLICATION NUMBER: US/10/821,568  
; CURRENT FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 09/816,763  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 92  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence for transcriptional factor P53  
US-10-821-568-92

Query Match 100.0%; Score 10; DB 17; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10  
|||||  
Db 1 RRRCWGYYY 10

RESULT 20  
US-10-821-568-92/c  
; Sequence 92, Application US/10821568  
; Publication No. US20040185497A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING. THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001DV1  
; CURRENT APPLICATION NUMBER: US/10/821,568  
; CURRENT FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 09/816,763  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 92  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence for transcriptional factor P53  
US-10-821-568-92

Query Match 100.0%; Score 10; DB 17; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10  
|||||  
Db 20 RRRCWGYYY 11

RESULT 21  
US-09-816-763-133  
; Sequence 133, Application US/09816763  
; Patent No. US20020110814A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING. THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001AUS  
; CURRENT APPLICATION NUMBER: US/09/816,763  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 133  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: P53 transcriptional factor consensus sequence  
; NAME/KEY: misc feature  
; LOCATION: (1)-(21)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-816-763-133

Query Match 100.0%; Score 10; DB 9; Length 21;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
| | | | | | | | | |  
Db 12 RRRCWGYYY 21

## RESULT 22

US-09-816-763-133/c  
; Sequence 133, Application US/09816763  
; Patent No. US20020110814A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANW212.001AUS  
; CURRENT APPLICATION NUMBER: US/09/816,763  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 133  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: P53 transcriptional factor consensus sequence  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(21)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-816-763-133

Query Match 100.0%; Score 10; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
| | | | | | | | | |  
Db 21 RRRCWGYYY 12

## RESULT 23

US-10-821-568-133  
; Sequence 133, Application US/10821568  
; Publication No. US20040185497A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANW212.001DVI  
; CURRENT APPLICATION NUMBER: US/10/821,568  
; PRIOR FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 09/816,763  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 133  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: consensus sequence for transcriptional factor p53

; NAME/KEY: misc\_feature  
; LOCATION: (1)...(21)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-821-568-133

Query Match 100.0%; Score 10; DB 17; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
| | | | | | | | | |  
Db 12 RRRCWGYYY 21

## RESULT 24

US-10-821-568-133/c  
; Sequence 133, Application US/10821568  
; Publication No. US20040185497A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANW212.001DVI  
; CURRENT APPLICATION NUMBER: US/10/821,568  
; PRIOR FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 09/816,763  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 133  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: consensus sequence for transcriptional factor p53  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(21)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-821-568-133

Query Match 100.0%; Score 10; DB 17; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10  
| | | | | | | | | |  
Db 21 RRRCWGYYY 12

## RESULT 25

US-09-816-763-134  
; Sequence 134, Application US/09816763  
; Patent No. US20020110814A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANW212.001AUS  
; CURRENT APPLICATION NUMBER: US/09/816,763  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-134

Query Match      100.0%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCCWGGYY 10
Db 13 RRRCCWGGYY 22

RESULT 26
US-09-816-763-134/c
; Sequence 134, Application US/09816763
; Publication No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANW212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-134

Query Match      100.0%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCCWGGYY 10
Db 22 RRRCCWGGYY 13

RESULT 27
US-10-821-568-134
; Sequence 134, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANW212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-134

Query Match      100.0%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCCWGGYY 10
Db 22 RRRCCWGGYY 13
```

```
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-134

Query Match      100.0%; Score 10; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCCWGGYY 10
Db 13 RRRCCWGGYY 22

RESULT 28
US-10-821-568-134/c
; Sequence 134, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANW212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-134

Query Match      100.0%; Score 10; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCCWGGYY 10
Db 22 RRRCCWGGYY 13

RESULT 29
US-09-816-763-135
; Sequence 135, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
```

```

; APPLICANT: Renard, Patricia
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-135

```

```

Query Match      100.0%; Score 10; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RRRCCWGGYY 10
    |||||
DB 14 RRRCCWGGYY 23

```

```

RESULT 30
US-09-816-763-135/c
; Sequence 135, Application US/09816763
; Patent No. US2002011081A1
; GENERAL INFORMATION:
; APPLICANT: Renard, Jose
; APPLICANT: Renard, Patricia
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-135

```

```

Query Match      100.0%; Score 10; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RRRCCWGGYY 10
    |||||
DB 23 RRRCCWGGYY 14

```

```

RESULT 31
US-10-821-568-135
; Sequence 135, Application US/10821568

```

```

; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Renard, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-135

```

```

Query Match      100.0%; Score 10; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RRRCCWGGYY 10
    |||||
DB 14 RRRCCWGGYY 23

```

```

RESULT 32
US-10-821-568-135/c
; Sequence 135, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Renard, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-135

```

```

Query Match      100.0%; Score 10; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy 1 RRCWGWYYY 10
    |||||
Db 23 RRCWGWYYY 14

RESULT 33
US-09-816-763-136
; Sequence 136, Application US/09816763
; Publication No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc feature
; LOCATION: (1)...(24)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-136

Query Match 100.0%; Score 10; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
    |||||
Db 15 RRCWGWYYY 24

RESULT 34
US-09-816-763-136/c
; Sequence 136, Application US/09816763
; Publication No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc feature
; LOCATION: (1)...(24)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-136

Query Match 100.0%; Score 10; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
    |||||
Db 15 RRCWGWYYY 24

RESULT 35
US-10-821-568-136
; Sequence 136, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(24)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-136

Query Match 100.0%; Score 10; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
    |||||
Db 15 RRCWGWYYY 24

RESULT 36
US-10-821-568-136/c
; Sequence 136, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 24
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(24)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-136

Query Match      100.0%; Score 10; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCRCWGGYY 10
Db 24 RRCRCWGGYY 15

RESULT 37
US-09-816-763-137
; Sequence 137, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-137

Query Match      100.0%; Score 10; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCRCWGGYY 10
Db 16 RRCRCWGGYY 25

RESULT 38
US-09-816-763-137/c
; Sequence 137, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-137

Query Match      100.0%; Score 10; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCRCWGGYY 10
Db 25 RRCRCWGGYY 16

RESULT 39
US-10-821-568-137
; Sequence 137, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001DVI
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-137

Query Match      100.0%; Score 10; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCRCWGGYY 10
Db 16 RRCRCWGGYY 25

RESULT 40
US-10-821-568-137/c
; Sequence 137, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
```

```
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-137
```

```
Query Match 100.0%; Score 10; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RRRCWGYYY 10
Db 25 RRRCWGYYY 16
```

## RESULT 41

```
US-09-816-763-138
; Sequence 138, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(26)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-138
```

```
Query Match 100.0%; Score 10; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RRRCWGYYY 10
Db 17 RRRCWGYYY 26
```

## RESULT 42

```
US-09-816-763-138/c
; Sequence 138, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(26)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-138
```

```
Query Match 100.0%; Score 10; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RRRCWGYYY 10
Db 26 RRRCWGYYY 17
```

## RESULT 43

```
US-10-821-568-138
; Sequence 138, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(26)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-138
```

```
Query Match 100.0%; Score 10; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RRRCWGYYY 10
Db 17 RRRCWGYYY 26
```

```
RESULT 44
US-10-821-568-138/c
; Sequence 139, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)..(26)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-138

Query Match      100.0%; Score 10; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRCWGWYYY 10
Db      26 RRCWGWYYY 17

RESULT 45
US-09-816-763-139
; Sequence 139, Application US/09816763
; Patent No. US200201108141
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(27)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-139

Query Match      100.0%; Score 10; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRCWGWYYY 10
Db      27 RRCWGWYYY 18

RESULT 46
US-09-816-763-139/c
; Sequence 139, Application US/09816763
; Patent No. US200201108141
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(27)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-139

Query Match      100.0%; Score 10; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRCWGWYYY 10
Db      27 RRCWGWYYY 18

RESULT 47
US-10-821-568-139
; Sequence 139, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
US-10-821-568-139
```



; LOCATION: (1)...(27)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-821-568-139

Query Match 100.0%; Score 10; DB 17; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10  
| | | | | | | | | |  
Db 18 RRRCWGYY 27

RESULT 48  
US-10-821-568-139/c  
; Sequence 139, Application US/10821568  
; Publication No. US20040185497A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001DV1  
; CURRENT APPLICATION NUMBER: US/10/821,568  
; PRIOR FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 09/816,763  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 139  
; LENGTH: 27

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(27)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-821-568-139

Query Match 100.0%; Score 10; DB 17; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10  
| | | | | | | | | |  
Db 27 RRRCWGYY 18

RESULT 49  
US-09-816-763-140  
; Sequence 140, Application US/09816763  
; Patent No. US20020110814A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001AUS  
; CURRENT APPLICATION NUMBER: US/09/816,763  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 140

; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: P53 transcriptional factor consensus sequence  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(28)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-816-763-140

Query Match 100.0%; Score 10; DB 9; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10  
| | | | | | | | | |  
Db 19 RRRCWGYY 28

RESULT 50  
US-09-816-763-140/c  
; Sequence 140, Application US/09816763  
; Patent No. US20020110814A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001AUS  
; CURRENT APPLICATION NUMBER: US/09/816,763  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 140  
; LENGTH: 28

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: P53 transcriptional factor consensus sequence  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(28)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-816-763-140

Query Match 100.0%; Score 10; DB 9; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10  
| | | | | | | | | |  
Db 28 RRRCWGYY 19

RESULT 51  
US-10-821-568-140  
; Sequence 140, Application US/10821568  
; Publication No. US20040185497A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001DV1  
; CURRENT APPLICATION NUMBER: US/10/821,568  
; CURRENT FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 09/816,763  
; PRIOR FILING DATE: 2001-03-23

```
/ PRIOR APPLICATION NUMBER: EP 00870057.7
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 140
/ LENGTH: 28
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: consensus sequence for transcriptional factor p53
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(28)
/ OTHER INFORMATION: n = A,T,C or G
US-10-821-568-140

Query Match      100.0%; Score 10; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
   |||||
Db 19 RRRRCWGGYY 28

RESULT 52
US-10-821-568-140/c
/ Sequence 140, Application US/10821568
/ Publication No. US20040185497A1
/ GENERAL INFORMATION:
/ APPLICANT: Remacle, Jose
/ APPLICANT: Renard, Patricia
/ APPLICANT: Art, Muriel
/ TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
/ TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
/ TITLE OF INVENTION: FACTORS
/ FILE REFERENCE: VANM212.001DV1
/ CURRENT APPLICATION NUMBER: US/10/821,568
/ CURRENT FILING DATE: 2004-04-08
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: EP 00870057.7
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 140
/ LENGTH: 28
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: consensus sequence for transcriptional factor p53
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(28)
/ OTHER INFORMATION: n = A,T,C or G
US-10-821-568-140

Query Match      100.0%; Score 10; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
   |||||
Db 28 RRRRCWGGYY 19

RESULT 53
US-09-816-763-141
/ Sequence 141, Application US/09816763
/ Patent No. US20020110814A1
/ GENERAL INFORMATION:
/ APPLICANT: Remacle, Jose
/ APPLICANT: Renard, Patricia
/ APPLICANT: Art, Muriel
/ TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
/ TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
/ TITLE OF INVENTION: FACTORS
/ FILE REFERENCE: VANM212.001AUS
/ CURRENT APPLICATION NUMBER: US/09/816,763
/ CURRENT FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: EP 00870057.7
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 141
/ LENGTH: 29
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: p53 transcriptional factor consensus sequence
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(29)
/ OTHER INFORMATION: n = A,T,C or G
US-09-816-763-141

Query Match      100.0%; Score 10; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
   |||||
Db 29 RRRRCWGGYY 20

RESULT 54
US-09-816-763-141/c
/ Sequence 141, Application US/09816763
/ Patent No. US20020110814A1
/ GENERAL INFORMATION:
/ APPLICANT: Remacle, Jose
/ APPLICANT: Renard, Patricia
/ APPLICANT: Art, Muriel
/ TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
/ TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
/ TITLE OF INVENTION: FACTORS
/ FILE REFERENCE: VANM212.001AUS
/ CURRENT APPLICATION NUMBER: US/09/816,763
/ CURRENT FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: EP 00870057.7
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 141
/ LENGTH: 29
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: p53 transcriptional factor consensus sequence
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(29)
/ OTHER INFORMATION: n = A,T,C or G
US-09-816-763-141

Query Match      100.0%; Score 10; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
   |||||
Db 29 RRRRCWGGYY 20

RESULT 55
US-10-821-568-141
/ Sequence 141, Application US/10821568
/ Publication No. US20040185497A1
```

;; GENERAL INFORMATION:  
;; APPLICANT: Remacle, Jose  
;; APPLICANT: Renard, Patricia  
;; APPLICANT: Art, Muriel  
;; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
;; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
;; FILE REFERENCE: VAMN212.001DV1  
;; CURRENT APPLICATION NUMBER: US/10/821,568  
;; PRIOR FILING DATE: 2004-04-08  
;; PRIOR APPLICATION NUMBER: US 09/816,763  
;; PRIOR FILING DATE: 2001-03-23  
;; PRIOR APPLICATION NUMBER: EP 00870057.7  
;; PRIOR FILING DATE: 2000-03-24  
;; NUMBER OF SEQ ID NOS: 150  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 141  
;; LENGTH: 29  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: consensus sequence for transcriptional factor p53  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(29)  
;; OTHER INFORMATION: n = A,T,C or G  
US-10-821-568-141

Query Match 100.0%; Score 10; DB 17; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10  
||| |||||

DB 20 RRRCWGYYY 29

RESULT 56  
US-10-821-568-141/c  
;; Sequence 141, Application US/10821568  
;; Publication No. US20040185497A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Remacle, Jose  
;; APPLICANT: Renard, Patricia  
;; APPLICANT: Art, Muriel  
;; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
;; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
;; FILE REFERENCE: VAMN212.001DV1  
;; CURRENT APPLICATION NUMBER: US/10/821,568  
;; PRIOR FILING DATE: 2004-04-08  
;; PRIOR APPLICATION NUMBER: US 09/816,763  
;; PRIOR FILING DATE: 2001-03-23  
;; PRIOR APPLICATION NUMBER: EP 00870057.7  
;; PRIOR FILING DATE: 2000-03-24  
;; NUMBER OF SEQ ID NOS: 150  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 141  
;; LENGTH: 29  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: consensus sequence for transcriptional factor p53  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(29)  
;; OTHER INFORMATION: n = A,T,C or G  
US-10-821-568-141

Query Match 100.0%; Score 10; DB 17; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10  
||| |||||

DB 29 RRRCWGYYY 20

RESULT 57  
US-09-816-763-142  
;; Sequence 142, Application US/09816763  
;; Patent No. US20020110814A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Remacle, Jose  
;; APPLICANT: Renard, Patricia  
;; APPLICANT: Art, Muriel  
;; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
;; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
;; FILE REFERENCE: VAMN212.001AUS  
;; CURRENT APPLICATION NUMBER: US/09/816,763  
;; CURRENT FILING DATE: 2001-03-23  
;; PRIOR APPLICATION NUMBER: EP 00870057.7  
;; PRIOR FILING DATE: 2000-03-24  
;; NUMBER OF SEQ ID NOS: 150  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 142  
;; LENGTH: 30  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: P53 transcriptional factor consensus sequence  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(30)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-816-763-142

Query Match 100.0%; Score 10; DB 9; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10  
||| |||||

DB 21 RRRCWGYYY 30

RESULT 58  
US-09-816-763-142/c  
;; Sequence 142, Application US/09816763  
;; Patent No. US20020110814A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Remacle, Jose  
;; APPLICANT: Renard, Patricia  
;; APPLICANT: Art, Muriel  
;; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
;; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
;; FILE REFERENCE: VAMN212.001AUS  
;; CURRENT APPLICATION NUMBER: US/09/816,763  
;; CURRENT FILING DATE: 2001-03-23  
;; PRIOR APPLICATION NUMBER: EP 00870057.7  
;; PRIOR FILING DATE: 2000-03-24  
;; NUMBER OF SEQ ID NOS: 150  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 142  
;; LENGTH: 30  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: P53 transcriptional factor consensus sequence  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)...(30)  
;; OTHER INFORMATION: n = A,T,C or G  
US-09-816-763-142

Query Match 100.0%; Score 10; DB 9; Length 30;

```
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
Db 30 RRCWGWYYY 21

RESULT 59
US-10-821-568-142
; Sequence 142, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(30)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-142

Query Match 100.0%; Score 10; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
Db 30 RRCWGWYYY 21

RESULT 60
US-10-821-568-142/c
; Sequence 142, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(30)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-142

Query Match 100.0%; Score 10; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
Db 21 RRCWGWYYY 30

RESULT 60
US-10-821-568-142/c
; Sequence 142, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(31)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-143

Query Match 100.0%; Score 10; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
Db 22 RRCWGWYYY 31

RESULT 62
US-09-816-763-143/c
; Sequence 143, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 143
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc.feature
; LOCATION: (1)...(31)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-143

Query Match      100.0%; Score 10; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      31 RRRCWGYY 22

RESULT 63
US-10-821-568-143
; Sequence 143, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc.feature
; LOCATION: (1)...(31)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-143

Query Match      100.0%; Score 10; DB 17; Length 31;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      31 RRRCWGYY 22

RESULT 64
US-10-821-568-143/c
; Sequence 143, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
```

```
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc.feature
; LOCATION: (1)...(31)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-143

Query Match      100.0%; Score 10; DB 17; Length 31;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      31 RRRCWGYY 22

RESULT 65
US-09-816-763-144
; Sequence 144, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc.feature
; LOCATION: (1)...(32)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-144

Query Match      100.0%; Score 10; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      23 RRRCWGYY 32

RESULT 66
US-09-816-763-144/c
; Sequence 144, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
```

```
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANN212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc feature
; LOCATION: (1)...(32)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-144
```

```
Query Match 100.0%; Score 10; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYY 10
Db 32 RRCWGWYY 23
```

```
RESULT 67
US-10-821-568-144
; Sequence 144, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANN212.001DVI
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(32)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-144
```

```
Query Match 100.0%; Score 10; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYY 10
Db 23 RRCWGWYY 32
```

```
RESULT 68
US-10-821-568-144/c
; Sequence 144, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANN212.001DVI
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(32)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-144
```

```
Query Match 100.0%; Score 10; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYY 10
Db 32 RRCWGWYY 23
```

```
RESULT 69
US-10-821-568-145
; Sequence 145, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANN212.001DVI
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(33)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-145
```



```
/ OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-10-017-178-5

Query Match          40.0%; Score 4; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WGYG 9
Db 6 WGYG 9

RESULT 74
US-10-017-178-5/c
; Sequence 5, Application US/10017178
; Publication No. US20020142287A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Hirotsuka
; APPLICANT: Moskal, Joseph R.
; TITLE OF INVENTION: High Throughput Assay to Detect Inhibitors of the MAP Kinase Path
; FILE REFERENCE: 99,123-D
; CURRENT APPLICATION NUMBER: US/10/017,178
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/255,548
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-10-017-178-5

Query Match          40.0%; Score 4; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCW 5
Db 9 RRCW 6

RESULT 75
US-10-636-065-212
; Sequence 212, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1,17,18
; OTHER INFORMATION: Y=um
; NAME/KEY: modified_base
; LOCATION: 19
; OTHER INFORMATION: Y=cm
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens
US-10-636-065-212

Query Match          40.0%; Score 4; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRG 4
Db 19 RRRG 16

RESULT 77
US-10-407-897-50
; Sequence 50, Application US/10407897
; Publication No. US20040072148A1
; GENERAL INFORMATION:
; APPLICANT: Ji, Jiuping
; APPLICANT: Manak, Mark
; APPLICANT: Gonzalez, Irene
; TITLE OF INVENTION: Simultaneous Detection of HBV, HCV, and HIV in Plasma Samples
; FILE REFERENCE: 1589.0280002
; CURRENT APPLICATION NUMBER: US/10/407,897
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 10/130,533
; PRIOR FILING DATE: 2002-11-17
; OTHER INFORMATION: PCT/ US00/31738
```



; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: US 60/165,916  
; PRIOR FILING DATE: 1999-11-17  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 50  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide Primer  
US-10-407-897-50

Query Match 40.0%; Score 4; DB 16; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCW 5  
Db 11 RRCW 14

## RESULT 78

US-10-407-897-50/c  
; Sequence 50, Application US/10407897  
; Publication No. US20040072148A1  
; GENERAL INFORMATION:  
; APPLICANT: Ji, Jiuping  
; APPLICANT: Gonzalez, Irene  
; TITLE OF INVENTION: Simultaneous Detection of HBV, HCV, and HIV in Plasma Samples  
; TITLE OF INVENTION: Using a Multiplex Capture Assay  
; FILE REFERENCE: 1589.0280002  
; CURRENT APPLICATION NUMBER: US/10/407,897  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: 10/130,533  
; PRIOR FILING DATE: 2002-11-17  
; PRIOR APPLICATION NUMBER: PCT/ US00/31738  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: US 60/165,916  
; PRIOR FILING DATE: 1999-11-17  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 50  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide Primer  
US-10-407-897-50

Query Match 40.0%; Score 4; DB 16; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WGYI 9  
Db 14 WGYI 11

## RESULT 79

US-10-225-519-16  
; Sequence 16, Application US/10225519  
; Publication No. US20030086940A1  
; GENERAL INFORMATION:  
; APPLICANT: Costa, Cristina  
; APPLICANT: Pizzolato, Maryellen C.  
; APPLICANT: Fodor, William L.  
; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CELL  
; TITLE OF INVENTION: EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM  
; FILE REFERENCE: 33-CIP  
; CURRENT APPLICATION NUMBER: US/10/225,519  
; CURRENT FILING DATE: 2002-08-20

; PRIOR APPLICATION NUMBER: US 09/928,267  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/29151  
; PRIOR FILING DATE: 2000-10-21  
; PRIOR APPLICATION NUMBER: US 60/161,186  
; PRIOR FILING DATE: 1999-10-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 5' forward primer.  
US-10-225-519-16

Query Match 40.0%; Score 4; DB 14; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10  
Db 19 GYYY 22

## RESULT 80

US-10-225-519-16/c  
; Sequence 16, Application US/10225519  
; Publication No. US20030086940A1  
; GENERAL INFORMATION:  
; APPLICANT: Costa, Cristina  
; APPLICANT: Pizzolato, Maryellen C.  
; APPLICANT: Fodor, William L.  
; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CELL  
; TITLE OF INVENTION: EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM  
; FILE REFERENCE: 33-CIP  
; CURRENT APPLICATION NUMBER: US/10/225,519  
; CURRENT FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: US 09/928,267  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/29151  
; PRIOR FILING DATE: 2000-10-21  
; PRIOR APPLICATION NUMBER: US 60/161,186  
; PRIOR FILING DATE: 1999-10-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 5' forward primer.  
US-10-225-519-16

Query Match 40.0%; Score 4; DB 14; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCR 4  
Db 22 RRCR 19

## RESULT 81

US-09-780-651-3  
; Sequence 3, Application US/09780651  
; Patent No. US20020048756A1  
; GENERAL INFORMATION:  
; APPLICANT: Robinson, Daniel  
; APPLICANT: Kung, Hsing-Jien  
; TITLE OF INVENTION: Analysis of Gene Family Expression  
; FILE REFERENCE: CASE-06110  
; CURRENT APPLICATION NUMBER: US/09/780,651

; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 09/073,407  
; PRIOR FILING DATE: 1998-05-06  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 3  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-780-651-3

Query Match 40.0%; Score 4; DB 9; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WGGY 8  
|||  
Db 16 WGGY 19

RESULT 82  
US-09-780-651-3/c  
; Sequence 3, Application US/09780651  
; Patent No. US20020048756A1  
; GENERAL INFORMATION:  
; APPLICANT: Robinson, Daniel  
; APPLICANT: Kung, Haing-Jien  
; TITLE OF INVENTION: Analysis of Gene Family Expression  
; FILE REFERENCE: CASE-06110  
; CURRENT APPLICATION NUMBER: US/09/780,651  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 09/073,407  
; PRIOR FILING DATE: 1998-05-06  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 3  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-780-651-3

Query Match 40.0%; Score 4; DB 9; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RCWW 6  
|||  
Db 19 RCWW 16

RESULT 83  
US-10-658-093-51  
; Sequence 51, Application US/10658093  
; Publication No. US20040115704A1  
; GENERAL INFORMATION:  
; APPLICANT: Daly, John Michael  
; TITLE OF INVENTION: Constructs for Gene Expression Analysis  
; FILE REFERENCE: 12177722  
; CURRENT APPLICATION NUMBER: US/10/658,093  
; CURRENT FILING DATE: 2003-09-09  
; PRIOR APPLICATION NUMBER: USSN 60/274770  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: PCT/AU02/00351  
; PRIOR FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 51  
; LENGTH: 30  
; TYPE: RNA

; ORGANISM: mammalian  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are  
; OTHER INFORMATION: selected from any nucleotide  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (19)..(19)  
; OTHER INFORMATION: n is a, c, g, or u  
US-10-658-093-51

Query Match 40.0%; Score 4; DB 17; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRC 4  
|||  
Db 21 RRRRC 24

RESULT 84  
US-10-658-093-51/c  
; Sequence 51, Application US/10658093  
; Publication No. US20040115704A1  
; GENERAL INFORMATION:  
; APPLICANT: Daly, John Michael  
; TITLE OF INVENTION: Constructs for Gene Expression Analysis  
; FILE REFERENCE: 12177722  
; CURRENT APPLICATION NUMBER: US/10/658,093  
; CURRENT FILING DATE: 2003-09-09  
; PRIOR APPLICATION NUMBER: USSN 60/274770  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: PCT/AU02/00351  
; PRIOR FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 51  
; LENGTH: 30  
; TYPE: RNA  
; ORGANISM: mammalian  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are  
; OTHER INFORMATION: selected from any nucleotide  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (19)..(19)  
; OTHER INFORMATION: n is a, c, g, or u  
US-10-658-093-51

Query Match 40.0%; Score 4; DB 17; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRC 4  
|||  
Db 14 RRRRC 11

RESULT 85  
US-10-658-093-52  
; Sequence 52, Application US/10658093  
; Publication No. US20040115704A1  
; GENERAL INFORMATION:  
; APPLICANT: Daly, John Michael  
; TITLE OF INVENTION: Constructs for Gene Expression Analysis  
; FILE REFERENCE: 12177722  
; CURRENT APPLICATION NUMBER: US/10/658,093  
; CURRENT FILING DATE: 2003-09-09  
; PRIOR APPLICATION NUMBER: USSN 60/274770  
; PRIOR FILING DATE: 2001-03-09

```

; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 30
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are
; OTHER INFORMATION: selected from any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is a, c, g, or t
US-10-658-093-52

```

```

Query Match      40.0%; Score 4; DB 17; Length 30;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RRRRC 4
      ||||
Db      21 RRRRC 24

```

```

RESULT 86
US-10-658-093-52/c
; Sequence 52, Application US/10658093
; Publication No. US20040115704A1
; GENERAL INFORMATION:
; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis
; FILE REFERENCE: 12177722
; CURRENT APPLICATION NUMBER: US/10/658,093
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: USSN 60/274770
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 30
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are
; OTHER INFORMATION: selected from any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is a, c, g, or t
US-10-658-093-52

```

```

Query Match      40.0%; Score 4; DB 17; Length 30;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RRRRC 4
      ||||
Db      14 RRRRC 11

```

```

RESULT 87
US-10-658-093-51
; Sequence 51, Application US/10658093
; Publication No. US20040209274A2
; GENERAL INFORMATION:

```

```

; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis
; FILE REFERENCE: 12177722
; CURRENT APPLICATION NUMBER: US/10/658,093
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: USSN 60/274770
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 30
; TYPE: RNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are
; OTHER INFORMATION: selected from any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is a, c, g, or u
US-10-658-093-51

```

```

Query Match      40.0%; Score 4; DB 18; Length 30;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RRRRC 4
      ||||
Db      21 RRRRC 24

```

```

RESULT 88
US-10-658-093-51/c
; Sequence 51, Application US/10658093
; Publication No. US20040209274A2
; GENERAL INFORMATION:
; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis
; FILE REFERENCE: 12177722
; CURRENT APPLICATION NUMBER: US/10/658,093
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: USSN 60/274770
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 30
; TYPE: RNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are
; OTHER INFORMATION: selected from any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is a, c, g, or u
US-10-658-093-51

```

```

Query Match      40.0%; Score 4; DB 18; Length 30;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RRRRC 4
      ||||
Db      14 RRRRC 11

```

## RESULT 89

US-10-658-093-52  
; Sequence 52, Application US/10658093  
; Publication No. US20040209274A2

## GENERAL INFORMATION:

; APPLICANT: Daly, John Michael  
; TITLE OF INVENTION: Constructs for Gene Expression Analysis

; FILE REFERENCE: 12177722

; CURRENT APPLICATION NUMBER: US/10/658,093

; CURRENT FILING DATE: 2003-09-09

; PRIOR APPLICATION NUMBER: USSN 60/274770

; PRIOR FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: PCT/AU02/00351

; PRIOR FILING DATE: 2001-03-08

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 52

; LENGTH: 30

; TYPE: DNA

; ORGANISM: mammalian

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (4)..(4)

; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are selected from any nucleotide

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (19)..(19)

; OTHER INFORMATION: n is a, c, g, or t

US-10-658-093-52

## Query Match

Best Local Similarity 40.0%; Score 4; DB 18; Length 30;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCR 4

Db 21 RRCR 24

## RESULT 90

US-10-658-093-52/c  
; Sequence 52, Application US/10658093  
; Publication No. US20040209274A2

## GENERAL INFORMATION:

; APPLICANT: Daly, John Michael

; TITLE OF INVENTION: Constructs for Gene Expression Analysis

; FILE REFERENCE: 12177722

; CURRENT APPLICATION NUMBER: US/10/658,093

; CURRENT FILING DATE: 2003-09-09

; PRIOR APPLICATION NUMBER: USSN 60/274770

; PRIOR FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: PCT/AU02/00351

; PRIOR FILING DATE: 2001-03-08

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 52

; LENGTH: 30

; TYPE: DNA

; ORGANISM: mammalian

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (4)..(4)

; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are selected from any nucleotide

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (19)..(19)

; OTHER INFORMATION: n is a, c, g, or t

US-10-658-093-52

## Query Match

Best Local Similarity 40.0%; Score 4; DB 18; Length 30;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCR 4

Db 14 RRCR 11

## RESULT 91

US-09-179-536B-320

; Sequence 320, Application US/09179536B

; Patent No. US20020042112A1

## GENERAL INFORMATION:

; APPLICANT: Hubert K ster

; David M. Lough

; Guobing Xiang

; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY

; NUMBER OF SEQUENCES: 320

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Heller Ehrman White & McAuliffe

; STREET: 4250 Executive Square, 7th Floor

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/20444

; FILING DATE: 06-NOV-1997

; APPLICATION NUMBER: 08/947,801

; FILING DATE: 08-Oct-97

; APPLICATION NUMBER: 08/933,792

; FILING DATE: 19-Sep-97

; APPLICATION NUMBER: 08/787,639

; FILING DATE: 23-Jan-97

; APPLICATION NUMBER: 08/786,988

; FILING DATE: 23-Jan-97

; APPLICATION NUMBER: 08/746,055

; FILING DATE: 06-No. US20020042112A1-96

; APPLICATION NUMBER: 08/746,036

; FILING DATE: 06-No. US20020042112A1-96

; APPLICATION NUMBER: 08/744,590

; FILING DATE: 06-No. US20020042112A1-96

; APPLICATION NUMBER: 08/744,481

; FILING DATE: 06-No. US20020042112A1-96

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L.

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 24736-2004B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 858-450-8400

; TELEFAX: 858-587-5360

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 320:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: <Unknown>

; ORIGINAL SOURCE:

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;
; SEQUENCE DESCRIPTION: SEQ ID NO: 320:
US-09-179-536B-320
Query Match 40.0%; Score 4; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWWG 7
Db 33 CWWG 36

RESULT 92
US-09-179-536B-320/c
; Sequence 320, Application US/09179536B
; Patent No. US20020042112A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K ster
; David M. Lough
; Guobing Xiang
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/179,536B
; FILING DATE: 26-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/20444
; FILING DATE: 06-NOV-1997
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/786,988
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/746,055
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/746,036
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-No. US20020042112A1-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 320:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
```

```
;
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 320:
US-09-179-536B-320
Query Match 40.0%; Score 4; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWWG 7
Db 36 CWWG 33

RESULT 93
US-09-297-576A-320
; Sequence 320, Application US/09297576A
; Publication No. US20030129589A1
; GENERAL INFORMATION:
; APPLICANT: KOSTER, Hubert
; APPLICANT: LITTLE, Daniel P.
; APPLICANT: BRAUN, Andreas
; APPLICANT: LOUGH, David M.
; APPLICANT: XIANG, Guobing
; APPLICANT: VAN DEN BOOM, Dirk
; APPLICANT: JURINKE, Christian
; APPLICANT: RUPPERT, Andreas
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/297,576A
; FILING DATE: 07-Jun-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/786,988
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/746,055
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/746,036
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-No. US20030129589A1-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-450-8499
; INFORMATION FOR SEQ ID NO: 320:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
```

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
US-09-297-576A-320

Query Match 40.0%; Score 4; DB 10; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWG 7  
Db 33 CWG 36

## RESULT 94

US-09-297-576A-320/c  
Sequence 320, Application US/09297576A  
Publication No US20030129589A1

## GENERAL INFORMATION:

APPLICANT: KOSTER, Hubert  
APPLICANT: LITTLE, Daniel P.  
APPLICANT: BRAUN, Andreas  
APPLICANT: LOUGH, David M.  
APPLICANT: XIANG, Guobing  
APPLICANT: VAN DEN BOOM, Dirk  
APPLICANT: JURINKE, Christian  
APPLICANT: RUPPERT, Andreas  
TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY  
NUMBER OF SEQUENCES: 320

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McAuliffe  
STREET: 4250 Executive Square, 7th Floor  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/297,576A  
FILING DATE: 07-Jun-2000

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/947,801  
FILING DATE: 08-Oct-97  
APPLICATION NUMBER: 08/933,792  
FILING DATE: 19-Sep-97  
APPLICATION NUMBER: 08/787,639  
FILING DATE: 23-Jan-97  
APPLICATION NUMBER: 08/786,988  
FILING DATE: 23-Jan-97  
APPLICATION NUMBER: 08/746,055  
FILING DATE: 06-No. US20030129589A1-96  
APPLICATION NUMBER: 08/746,036  
FILING DATE: 06-No. US20030129589A1-96  
APPLICATION NUMBER: 08/744,590  
FILING DATE: 06-No. US20030129589A1-96  
APPLICATION NUMBER: 08/744,481  
FILING DATE: 06-No. US20030129589A1-96  
ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24736-2004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-450-8400

TELEFAX: 858-450-8499  
INFORMATION FOR SEQ ID NO: 320:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
US-09-297-576A-320

Query Match 40.0%; Score 4; DB 10; Length 38;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWG 7  
Db 36 CWG 33

## RESULT 95

US-10-293-252C-5  
Sequence 5, Application US/10293252C  
Publication No. US20040103449A1

## GENERAL INFORMATION:

APPLICANT: Xu, Dongmei  
TITLE OF INVENTION: Identification and Use of Cytochrome  
FILE REFERENCE: 78127  
CURRENT APPLICATION NUMBER: US/10/293,252C  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: 60/363,684  
PRIOR FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/347,444  
PRIOR FILING DATE: 2002-01-11  
PRIOR APPLICATION NUMBER: 60/337,684  
PRIOR FILING DATE: 2001-11-13  
NUMBER OF SEQ ID NOS: 152  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 4  
TYPE: DNA  
ORGANISM: Nicotiana

## US-10-293-252C-5

Query Match 30.0%; Score 3; DB 17; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
Db 2 RRC 4

## RESULT 96

US-10-293-252C-5/c  
Sequence 5, Application US/10293252C  
Publication No. US20040103449A1

## GENERAL INFORMATION:

APPLICANT: Xu, Dongmei  
TITLE OF INVENTION: Identification and Use of Cytochrome  
FILE REFERENCE: 78127  
CURRENT APPLICATION NUMBER: US/10/293,252C  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: 60/363,684  
PRIOR FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/347,444  
PRIOR FILING DATE: 2002-01-11  
PRIOR APPLICATION NUMBER: 60/337,684

; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 152  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 4  
; TYPE: DNA  
; ORGANISM: Nicotiana  
US-10-293-252C-5

Query Match 30.0%; Score 3; DB 17; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYI 9  
|||  
Db 4 GYI 2

RESULT 97  
US-10-340-861B-5  
; Sequence 5, Application US/10340861B  
; Publication No. US20040111759A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Dongmei  
; TITLE OF INVENTION: Identification and Use of Cytochrome  
; FILE REFERENCE: 78406  
; CURRENT APPLICATION NUMBER: US/10/340,861B  
; CURRENT FILING DATE: 2003-01-10  
; PRIOR APPLICATION NUMBER: 10/293,252  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 60/363,684  
; PRIOR FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 60/347,444  
; PRIOR FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: 60/337,684  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 4  
; TYPE: DNA  
; ORGANISM: Nicotiana  
US-10-340-861B-5

Query Match 30.0%; Score 3; DB 17; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
|||  
Db 2 RRC 4

RESULT 98  
US-10-340-861B-5/c  
; Sequence 5, Application US/10340861B  
; Publication No. US20040111759A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Dongmei  
; TITLE OF INVENTION: Identification and Use of Cytochrome  
; FILE REFERENCE: 78406  
; CURRENT APPLICATION NUMBER: US/10/340,861B  
; CURRENT FILING DATE: 2003-01-10  
; PRIOR APPLICATION NUMBER: 10/293,252  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 60/363,684  
; PRIOR FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 60/347,444  
; PRIOR FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: 60/337,684  
; PRIOR FILING DATE: 2001-11-13

; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 4  
; TYPE: DNA  
; ORGANISM: Nicotiana  
US-10-340-861B-5

Query Match 30.0%; Score 3; DB 17; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYI 9  
|||  
Db 4 GYI 2

RESULT 99  
US-10-253-117-1  
; Sequence 1, Application US/10253117  
; Publication No. US20030119773A1  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eyal R.  
; APPLICANT: KOBAYASHI, Hiroko  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE  
; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/10/253,117  
; CURRENT FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: US/09/347,343  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-10-253-117-1

Query Match 30.0%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
|||  
Db 1 RRC 3

RESULT 100  
US-10-253-117-1/c  
; Sequence 1, Application US/10253117  
; Publication No. US20030119773A1  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eyal R.  
; APPLICANT: KOBAYASHI, Hiroko  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE  
; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/10/253,117  
; CURRENT FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: US/09/347,343  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-10-253-117-1

Query Match 30.0%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4

```
Db          6 RRC 4
|||
RESULT 101
US-10-253-117-2
; Sequence 2, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-2
Query Match          30.0%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          7 GY 9
|||
Db          4 GY 6
|||
RESULT 102
US-10-253-117-2/c
; Sequence 2, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-2
Query Match          30.0%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          7 GY 9
|||
Db          4 GY 6
|||
RESULT 103
US-10-253-117-2
; Sequence 2, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-2
Query Match          30.0%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          2 RRC 4
|||
Db          6 RRC 4
|||
RESULT 104
US-10-290-545-27/c
; Sequence 27, Application US/10290545
; Publication No. US20030125292A1
; GENERAL INFORMATION:
; APPLICANT: Klimuk, Sandy
; APPLICANT: Yuan, Zuan-Ning
; TITLE OF INVENTION: Improved Mucosal Vaccines and Methods for Using the Same
; FILE REFERENCE: A-71854/TAL/AXG
; CURRENT APPLICATION NUMBER: US/10/290,545
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-290-545-27
Query Match          30.0%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          2 RRC 4
|||
Db          1 RRC 3
|||
RESULT 105
US-10-437-263-27
; Sequence 27, Application US/10437263
; Publication No. US20040009943A1
; GENERAL INFORMATION:
; APPLICANT: Semple, Sean
; APPLICANT: Tam, Ying K.
; APPLICANT: Chikh, Ghania
; APPLICANT: Hope, Michael J.
; TITLE OF INVENTION: PATHOGEN VACCINES AND METHODS FOR USING THE SAME
; FILE REFERENCE: A-72216/TAL
; CURRENT APPLICATION NUMBER: US/10/437,263
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/454,298
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 34
```



; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-437-263-27

Query Match 30.0%; Score 3; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
|||  
Db 1 RRC 3

## RESULT 106

US-10-437-263-27/c  
; Sequence 27, Application US/10437263  
; Publication No. US20040009943A1  
; GENERAL INFORMATION:

; APPLICANT: Semple, Sean  
; APPLICANT: Tam, Ying K.  
; APPLICANT: Klimuk, Sandra  
; APPLICANT: Chikh, Ghania  
; APPLICANT: Hope, Michael J.  
; TITLE OF INVENTION: PATHOGEN VACCINES AND METHODS FOR USING THE SAME  
; FILE REFERENCE: A-72216/TAL  
; CURRENT APPLICATION NUMBER: US/10/437,263  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,343  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/460,646  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 60/454,298  
; PRIOR FILING DATE: 2003-03-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-437-263-27

Query Match 30.0%; Score 3; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
|||  
Db 6 RRC 4

## RESULT 107

US-10-437-275-27  
; Sequence 27, Application US/10437275  
; Publication No. US20040009944A1  
; GENERAL INFORMATION:

; APPLICANT: Semple, Sean  
; APPLICANT: Tam, Ying K.  
; APPLICANT: Klimuk, Sandra  
; APPLICANT: Chikh, Ghania  
; TITLE OF INVENTION: METHYLATED IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND METHODS OF  
; FILE REFERENCE: A-72158/TAL  
; CURRENT APPLICATION NUMBER: US/10/437,275  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,343  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/460,646

; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/290,545  
; PRIOR FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-437-275-27

Query Match 30.0%; Score 3; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
|||  
Db 1 RRC 3

## RESULT 108

US-10-437-275-27/c  
; Sequence 27, Application US/10437275  
; Publication No. US20040009944A1  
; GENERAL INFORMATION:

; APPLICANT: Tam, Ying K.  
; APPLICANT: Semple, Sean  
; APPLICANT: Klimuk, Sandra  
; APPLICANT: Chikh, Ghania  
; TITLE OF INVENTION: METHYLATED IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND METHODS OF  
; FILE REFERENCE: A-72158/TAL  
; CURRENT APPLICATION NUMBER: US/10/437,275  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,343  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/460,646  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/290,545  
; PRIOR FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-437-275-27

Query Match 30.0%; Score 3; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
|||  
Db 6 RRC 4

## RESULT 109

US-10-437-258-27  
; Sequence 27, Application US/10437258  
; Publication No. US20040013649A1  
; GENERAL INFORMATION:

; APPLICANT: Tam, Ying K.  
; APPLICANT: Semple, Sean  
; APPLICANT: Klimuk, Sandra  
; APPLICANT: Chikh, Ghania  
; TITLE OF INVENTION: CANCER VACCINES AND METHODS OF USING THE SAME  
; FILE REFERENCE: A-72252/TAL  
; CURRENT APPLICATION NUMBER: US/10/437,258



```
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: Ets-1
US-09-816-763-32
```

```
Query Match 30.0%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 6 WGY 8
|||
Db 6 WGY 8
```

```
RESULT 114
US-09-816-763-32/c
; Sequence 32, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: Ets-1
US-09-816-763-32
```

```
Query Match 30.0%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 RCW 5
|||
Db 8 RCW 6
```

```
RESULT 115
US-09-798-883B-56
; Sequence 56, Application US/09798883B
; Publication No. US20030159159A1
; GENERAL INFORMATION:
; APPLICANT: LINNIK, Matthew
; APPLICANT: RACKE, Margaret
; APPLICANT: KRAKOWSKY, Joan
; APPLICANT: SUBRAMANIAM, Arun
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and Exon 3 Promoters
; FILE REFERENCE: HMR2002C US DIV
```

```
; CURRENT APPLICATION NUMBER: US/09/798,883B
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Binding Motif in Human Nerve Growth Factor Exon 1 and 3
; OTHER INFORMATION: Promoter
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: w=a or t
US-09-798-883B-56
```

```
Query Match 30.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 5 WGW 7
|||
Db 6 WGW 8
```

```
RESULT 116
US-09-798-883B-56/c
; Sequence 56, Application US/09798883B
; Publication No. US20030159159A1
; GENERAL INFORMATION:
; APPLICANT: LINNIK, Matthew
; APPLICANT: RACKE, Margaret
; APPLICANT: KRAKOWSKY, Joan
; APPLICANT: SUBRAMANIAM, Arun
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and Exon 3 Promoters
; FILE REFERENCE: HMR2002C US DIV
; CURRENT APPLICATION NUMBER: US/09/798,883B
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Binding Motif in Human Nerve Growth Factor Exon 1 and 3
; OTHER INFORMATION: Promoter
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: w=a or t
US-09-798-883B-56
```

```
Query Match 30.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 4 CWW 6
|||
Db 8 CWW 6
```

```
RESULT 117
US-09-326-885-56
; Sequence 56, Application US/09326885
; Publication No. US20030192065A1
; GENERAL INFORMATION:
; APPLICANT: Linnik, Matthew D
; APPLICANT: Racke, Margaret M
; APPLICANT: Krakowsky, Joan M
; APPLICANT: Subramaniam, Arun
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and
; NUMBER OF SEQUENCES: 84
; Exon 3 Promoters
```

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hoechst Marion Roussel, Inc.
/ STREET: 2110 East Galbraith Road, P.O. Box 156300
/ CITY: Cincinnati
/ STATE: Ohio
/ COUNTRY: United States of America
/ ZIP: 45215-6300
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/326,885
/ FILING DATE: 07-Jun-1999
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/020,179
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 60/038,212
/ FILING DATE: 06-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Payne, T. Helen
/ REGISTRATION NUMBER: 36,889
/ REFERENCE/DOCKET NUMBER: HMR2002A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 513 948-7183
/ TELEFAX: 513 948-7961/4681
/ TELEX: 214320
/
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-326-885-56

Query Match 30.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WVG 7
   |||
Db 6 WVG 8

RESULT 118
US-09-326-885-56/c
; Sequence 56, Application US/09126885
; Publication No. US20030192065A1
; GENERAL INFORMATION:
; APPLICANT: Linnik, Matthew D
; Racke, Margaret M
; Krakowsky, Joan M
; Subramaniam, Arun
;
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and
;
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoechst Marion Roussel, Inc.
; STREET: 2110 East Galbraith Road, P.O. Box 156300
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: United States of America
; ZIP: 45215-6300
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
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```
/
/ APPLICATION NUMBER: US/09/326,885
/ FILING DATE: 07-Jun-1999
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/020,179
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 60/038,212
/ FILING DATE: 06-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Payne, T. Helen
/ REGISTRATION NUMBER: 36,889
/ REFERENCE/DOCKET NUMBER: HMR2002A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 513 948-7183
/ TELEFAX: 513 948-7961/4681
/ TELEX: 214320
/
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-326-885-56

Query Match 30.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWV 6
   |||
Db 8 CWV 6

RESULT 119
US-10-253-117-3
; Sequence 3, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-3

Query Match 30.0%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
   |||
Db 1 RRC 3

RESULT 120
US-10-253-117-3/c
; Sequence 3, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
```

; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/10/253,117  
; CURRENT FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: US/09/347,343  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-10-253-117-3

Query Match 30.0%; Score 3; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
|||  
Db 6 RRC 4

## RESULT 121

US-10-253-117-4  
; Sequence 4, Application US/10253117  
; Publication No. US20030119773A1  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eval R.  
; APPLICANT: KOBAYASHI, Hiroko  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE  
; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/10/253,117  
; CURRENT FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: US/09/347,343  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-10-253-117-4

Query Match 30.0%; Score 3; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 9  
|||  
Db 4 GY 6

## RESULT 122

US-10-253-117-4/c  
; Sequence 4, Application US/10253117  
; Publication No. US20030119773A1  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, Eval R.  
; APPLICANT: KOBAYASHI, Hiroko  
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE  
; FILE REFERENCE: 30448.64US01  
; CURRENT APPLICATION NUMBER: US/10/253,117  
; CURRENT FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: US/09/347,343  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: synthetic oligonucleotide  
US-10-253-117-4

Query Match 30.0%; Score 3; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4  
|||  
Db 6 RRC 4

## RESULT 123

US-10-821-568-32  
; Sequence 32, Application US/10821568  
; Publication No. US20040185497A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANW212.001DV1  
; CURRENT APPLICATION NUMBER: US/10/821,568  
; CURRENT FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 09/816,763  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence for transcriptional factor  
; OTHER INFORMATION: Ets-1  
US-10-821-568-32

Query Match 30.0%; Score 3; DB 17; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WGY 8  
|||  
Db 6 WGY 8

## RESULT 124

US-10-821-568-32/c  
; Sequence 32, Application US/10821568  
; Publication No. US20040185497A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANW212.001DV1  
; CURRENT APPLICATION NUMBER: US/10/821,568  
; CURRENT FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 09/816,763  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence for transcriptional factor

/ OTHER INFORMATION: Ets-1  
US-10-821-568-32

Query Match 30.0%; Score 3; DB 17; Length 8;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RCW 5  
Db 8 RCW 6

## RESULT 125

US-09-772-719-23  
; Sequence 23, Application US/09772719  
; Patent No. US20020137910A1

## GENERAL INFORMATION:

; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-JAN-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034

; INFORMATION FOR SEQ ID NO: 23:

; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Initiator consensus sequence  
US-09-772-719-23

Query Match 30.0%; Score 3; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
Db 1 YYY 3

## RESULT 126

US-09-772-719-23/C  
; Sequence 23, Application US/09772719  
; Patent No. US20020137910A1

/ GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-JAN-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Initiator consensus sequence  
US-09-772-719-23

Query Match 30.0%; Score 3; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
Db 10 RRR 8

## RESULT 127

US-09-967-237-23  
; Sequence 23, Application US/09967237  
; Publication No. US20030049828A1

## GENERAL INFORMATION:

; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; FILE REFERENCE: D-0021.5B-2  
; CURRENT APPLICATION NUMBER: US/09/967,237  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 09/178,115  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: DNA

; ORGANISM: HUMAN



```

; PRIOR APPLICATION NUMBER: US 08/167,628
; PRIOR FILING DATE: 1993-12-14
; PRIOR APPLICATION NUMBER: US 07/752,427
; PRIOR FILING DATE: 1991-08-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Serum response element
US-10-338-587A-14

```

```

Query Match          30.0%; Score 3; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 4 CW 6
Db 2 CW 4

```

## RESULT 132

```

US-10-338-587A-14/c
; Sequence 14, Application US/10338587A
; Publication No. US20040005319A1
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF SOUTH FLORIDA
; APPLICANT: GROTEENDORST, Gary R.
; APPLICANT: BRADHAM, Douglass M.
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; FILE REFERENCE: USF1100-15
; CURRENT APPLICATION NUMBER: US/10/338,587A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 09/054,363
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: US 08/459,717
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/386,680
; PRIOR FILING DATE: 1995-02-10
; PRIOR APPLICATION NUMBER: US 08/167,628
; PRIOR FILING DATE: 1993-12-14
; PRIOR APPLICATION NUMBER: US 07/752,427
; PRIOR FILING DATE: 1991-08-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Serum response element
US-10-338-587A-14

```

```

Query Match          30.0%; Score 3; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 4 CW 6
Db 9 CW 7

```

## RESULT 133

```

US-10-172-526-15
; Sequence 15, Application US/10172526
; Publication No. US20040006783A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Zhenbiao
; APPLICANT: Bailey-Serres, Julia
; APPLICANT: Baxter-Burrell, Airica
; APPLICANT: Wu, Guang

```

```

; APPLICANT: Vernoud, Vanessa
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Compositions and Methods for Modulating RopGTPase
; TITLE OF INVENTION: Activity in Plants
; FILE REFERENCE: 023070-126000US
; CURRENT APPLICATION NUMBER: US/10/172,526
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:antioxidant
; OTHER INFORMATION: response element (ARE) consensus sequence
US-10-172-526-15

```

```

Query Match          30.0%; Score 3; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 WW 7
Db 7 WW 9

```

## RESULT 134

```

US-10-172-526-15/c
; Sequence 15, Application US/10172526
; Publication No. US20040006783A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Zhenbiao
; APPLICANT: Bailey-Serres, Julia
; APPLICANT: Baxter-Burrell, Airica
; APPLICANT: Wu, Guang
; APPLICANT: Vernoud, Vanessa
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Compositions and Methods for Modulating RopGTPase
; TITLE OF INVENTION: Activity in Plants
; FILE REFERENCE: 023070-126000US
; CURRENT APPLICATION NUMBER: US/10/172,526
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:antioxidant
; OTHER INFORMATION: response element (ARE) consensus sequence
US-10-172-526-15

```

```

Query Match          30.0%; Score 3; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 4 CW 6
Db 9 CW 7

```

## RESULT 135

```

US-10-689-006-32
; Sequence 32, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72

```



; CURRENT APPLICATION NUMBER: US/10/689,006  
; CURRENT FILING DATE: 2003-10-20  
; PRIOR APPLICATION NUMBER: US 09/914,605  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 10/259,087  
; PRIOR FILING DATE: 2002-09-27  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Serine-glycine-poly-tyrosine linking peptide  
US-10-689-006-32

Query Match 30.0%; Score 3; DB 18; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
|||  
Db 6 YYY 8

RESULT 136  
US-10-689-006-32/c  
; Sequence 32, Application US/10689006  
; Publication No. US20040191249A1  
; GENERAL INFORMATION:  
; APPLICANT: Vanderbilt University  
; APPLICANT: Hallahan, Dennis E  
; APPLICANT: Mernaugh, Raymond  
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS  
; FILE REFERENCE: 1242/72  
; CURRENT APPLICATION NUMBER: US/10/689,006  
; CURRENT FILING DATE: 2003-10-20  
; PRIOR APPLICATION NUMBER: US 09/914,605  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 10/259,087  
; PRIOR FILING DATE: 2002-09-27  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Serine-glycine-poly-tyrosine linking peptide  
US-10-689-006-32

Query Match 30.0%; Score 3; DB 18; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
|||  
Db 10 RRR 8

RESULT 137  
US-10-888-694-23  
; Sequence 23, Application US/10888694  
; Publication No. US20050003425A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 465 California Street, Suite 450

; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/888,694  
; FILING DATE: 08-Jul-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-Jan-2001  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3A-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Initiator consensus sequence  
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-10-888-694-23

Query Match 30.0%; Score 3; DB 18; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
|||  
Db 1 YYY 3

RESULT 138  
US-10-888-694-23/c  
; Sequence 23, Application US/10888694  
; Publication No. US20050003425A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 465 California Street, Suite 450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/888,694  
; FILING DATE: 08-Jul-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719

```

/ FILING DATE: 30-Jan-2001
/ APPLICATION NUMBER: US 08/485,049
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lauder, Leona L.
/ REGISTRATION NUMBER: 30,863
/ REFERENCE/DOCKET NUMBER: D-0021.3A-2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-981-2034
/ TELEFAX: 415-981-0332
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ DESCRIPTION: Initiator consensus sequence
/ SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-888-694-23

Query Match          30.0%; Score 3; DB 18; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 10 RRR 8

RESULT 139
US-10-359-050-3
/ Sequence 3, Application US/10359050
/ Publication No. US20030186291A1
/ GENERAL INFORMATION:
/ APPLICANT: EXELIXIS DEUTSCHLAND GMBH
/ TITLE OF INVENTION: GENETICALLY ENGINEERED PHIC31-INTEGRASE GENES
/ FILE REFERENCE: AR03-001
/ CURRENT APPLICATION NUMBER: US/10/359,050
/ CURRENT FILING DATE: 2003-02-05
/ PRIOR APPLICATION NUMBER: US 60/354,741
/ PRIOR FILING DATE: 2002-02-06
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Splice acceptor sequence
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(12)
/ OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-3

Query Match          30.0%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 140
US-10-359-050-3/c
/ Sequence 3, Application US/10359050
/ Publication No. US20030186291A1
/ GENERAL INFORMATION:
/ APPLICANT: EXELIXIS DEUTSCHLAND GMBH
/ TITLE OF INVENTION: GENETICALLY ENGINEERED PHIC31-INTEGRASE GENES
/ FILE REFERENCE: AR03-001
/ CURRENT APPLICATION NUMBER: US/10/359,050
/ CURRENT FILING DATE: 2003-02-05
/ PRIOR APPLICATION NUMBER: US 60/354,741
/ PRIOR FILING DATE: 2002-02-06
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Splice acceptor site.
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(12)
/ OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-4

Query Match          30.0%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 142
US-10-359-050-4/c
/ Sequence 4, Application US/10359050
/ Publication No. US20030186291A1
/ GENERAL INFORMATION:
/ APPLICANT: EXELIXIS DEUTSCHLAND GMBH
/ TITLE OF INVENTION: GENETICALLY ENGINEERED PHIC31-INTEGRASE GENES
/ FILE REFERENCE: AR03-001
/ CURRENT APPLICATION NUMBER: US/10/359,050
/ CURRENT FILING DATE: 2003-02-05
/ PRIOR APPLICATION NUMBER: US 60/354,741
/ PRIOR FILING DATE: 2002-02-06
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Splice acceptor site.
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(12)
/ OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-4

```

```

/ CURRENT APPLICATION NUMBER: US/10/359,050
/ CURRENT FILING DATE: 2003-02-05
/ PRIOR APPLICATION NUMBER: US 60/354,741
/ PRIOR FILING DATE: 2002-02-06
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Splice acceptor sequence
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(12)
/ OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-3

Query Match          30.0%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 7 RRR 5

RESULT 141
US-10-359-050-4
/ Sequence 4, Application US/10359050
/ Publication No. US20030186291A1
/ GENERAL INFORMATION:
/ APPLICANT: EXELIXIS DEUTSCHLAND GMBH
/ TITLE OF INVENTION: GENETICALLY ENGINEERED PHIC31-INTEGRASE GENES
/ FILE REFERENCE: AR03-001
/ CURRENT APPLICATION NUMBER: US/10/359,050
/ CURRENT FILING DATE: 2003-02-05
/ PRIOR APPLICATION NUMBER: US 60/354,741
/ PRIOR FILING DATE: 2002-02-06
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Splice acceptor site.
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(12)
/ OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-4

Query Match          30.0%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 142
US-10-359-050-4/c
/ Sequence 4, Application US/10359050
/ Publication No. US20030186291A1
/ GENERAL INFORMATION:
/ APPLICANT: EXELIXIS DEUTSCHLAND GMBH
/ TITLE OF INVENTION: GENETICALLY ENGINEERED PHIC31-INTEGRASE GENES
/ FILE REFERENCE: AR03-001
/ CURRENT APPLICATION NUMBER: US/10/359,050
/ CURRENT FILING DATE: 2003-02-05
/ PRIOR APPLICATION NUMBER: US 60/354,741
/ PRIOR FILING DATE: 2002-02-06
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Splice acceptor site.
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(12)
/ OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-4

```

; PRIOR FILING DATE: 2002-02-06  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Splice acceptor site.  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(12)  
; OTHER INFORMATION: Y is T or C; N is A, C, G, or T.  
US-10-359-050-4

Query Match 30.0%; Score 3; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
|||  
Db 7 RRR 5

RESULT 143  
US-10-300-011-78  
; Sequence 78, Application US/10300011  
; Publication No. US20030235890A1  
; GENERAL INFORMATION:  
; APPLICANT: WYLLIE, DAVID  
; APPLICANT: DUFF, GORDON W.  
; APPLICANT: AZIZ, NAZNEEN  
; APPLICANT: Hsieh, Chung Ming  
; APPLICANT: Kornman, Kenneth S.  
; TITLE OF INVENTION: FUNCTIONAL POLYMORPHISMS OF THE INTERLEUKIN-1 LOCUS  
; TITLE OF INVENTION: AFFECTING TRANSCRIPTION AND SUSCEPTIBILITY TO  
; FILE REFERENCE: MSA-024.01  
; CURRENT APPLICATION NUMBER: US/10/300,011  
; CURRENT FILING DATE: 2002-11-19  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 78  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: consensus sequence  
; NAME/KEY: modified\_base  
; LOCATION: (6)  
; OTHER INFORMATION: a, t, c or g  
US-10-300-011-78

Query Match 30.0%; Score 3; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
|||  
Db 7 YYY 9

RESULT 144  
US-10-300-011-78/c  
; Sequence 78, Application US/10300011  
; Publication No. US20030235890A1  
; GENERAL INFORMATION:  
; APPLICANT: WYLLIE, DAVID  
; APPLICANT: DUFF, GORDON W.  
; APPLICANT: AZIZ, NAZNEEN  
; APPLICANT: Hsieh, Chung Ming

; APPLICANT: Kornman, Kenneth S.  
; TITLE OF INVENTION: FUNCTIONAL POLYMORPHISMS OF THE INTERLEUKIN-1 LOCUS  
; TITLE OF INVENTION: AFFECTING TRANSCRIPTION AND SUSCEPTIBILITY TO  
; FILE REFERENCE: MSA-024.01  
; CURRENT APPLICATION NUMBER: US/10/300,011  
; CURRENT FILING DATE: 2002-11-19  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 78  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: consensus sequence  
; NAME/KEY: modified\_base  
; LOCATION: (6)  
; OTHER INFORMATION: a, t, c or g  
US-10-300-011-78

Query Match 30.0%; Score 3; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
|||  
Db 9 RRR 7

RESULT 145  
US-09-816-763-67  
; Sequence 67, Application US/09816763  
; Patent No. US20020110814A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Art, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001AUS  
; CURRENT APPLICATION NUMBER: US/09/816,763  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 67  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence for transcriptional factor  
; OTHER INFORMATION: MBF-1  
US-09-816-763-67

Query Match 30.0%; Score 3; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
|||  
Db 11 YYY 13

RESULT 146  
US-09-816-763-67/c  
; Sequence 67, Application US/09816763  
; Patent No. US20020110814A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose

```

; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: MBF-1
US-09-816-763-67

```

```

Query Match      30.0%; Score 3; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RRR 3
      |||
Db     13 RRR 11

```

```

RESULT 147
US-10-602-837-15
; Sequence 15, Application US/10602837
; Publication No. US20040053310A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Hua
; APPLICANT: Lis, John T.
; TITLE OF INVENTION: EXHAUSTIVE SELECTION OF RNA APTAMERS AGAINST COMPLEX
; TITLE OF INVENTION: TARGETS
; FILE REFERENCE: 19603/3921
; CURRENT APPLICATION NUMBER: US/10/602,837
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/391,255
; PRIOR FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2)
; OTHER INFORMATION: N at positions 1-2 can be A, T, G, or C
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (6)..(8)
; OTHER INFORMATION: W at positions 6-8 can be A or T
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (12)..(13)
; OTHER INFORMATION: N at positions 12-13 can be A, T, G, or C
US-10-602-837-15

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```

Query Match      30.0%; Score 3; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      4 CWW 6
      |||
Db     5 CWW 7

```

```

RESULT 148
US-10-602-837-15/c
; Sequence 15, Application US/10602837
; Publication No. US20040053310A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Hua
; APPLICANT: Lis, John T.
; TITLE OF INVENTION: EXHAUSTIVE SELECTION OF RNA APTAMERS AGAINST COMPLEX
; TITLE OF INVENTION: TARGETS
; FILE REFERENCE: 19603/3921
; CURRENT APPLICATION NUMBER: US/10/602,837
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/391,255
; PRIOR FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2)
; OTHER INFORMATION: N at positions 1-2 can be A, T, G, or C
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (6)..(8)
; OTHER INFORMATION: W at positions 6-8 can be A or T
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (12)..(13)
; OTHER INFORMATION: N at positions 12-13 can be A, T, G, or C
US-10-602-837-15

```

```

Query Match      30.0%; Score 3; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 WWG 7
      |||
Db     7 WWG 5

```

```

RESULT 149
US-10-821-568-67
; Sequence 67, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Renard, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor

```

```
; OTHER INFORMATION: MBF-1
US-10-821-568-67

Query Match      30.0%; Score 3; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
Db      11 YYY 13
      |||

RESULT 150
US-10-821-568-67/c
; Sequence 67, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANW212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: MBF-1
US-10-821-568-67

Query Match      30.0%; Score 3; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
Db      13 RRR 11
      |||

RESULT 151
US-09-802-807-7
; Sequence 7, Application US/09802807
; Patent No. US2001003404A1
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
; FILE REFERENCE: 07236/016001
; CURRENT APPLICATION NUMBER: US/09/802,807
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/084,663
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (14)
; OTHER INFORMATION: n = A,T,C or G

; OTHER INFORMATION: MBF-1
US-10-821-568-67

Query Match      30.0%; Score 3; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
Db      13 RRR 11
      |||

RESULT 151
US-09-802-807-7
; Sequence 7, Application US/09802807
; Patent No. US2001003404A1
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
; FILE REFERENCE: 07236/016001
; CURRENT APPLICATION NUMBER: US/09/802,807
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/084,663
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (14)

; OTHER INFORMATION: n = A,T,C or G
US-09-802-807-7

Query Match      30.0%; Score 3; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
Db      1 YYY 3
      |||

RESULT 152
US-09-802-807-7/c
; Sequence 7, Application US/09802807
; Patent No. US2001003404A1
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
; FILE REFERENCE: 07236/016001
; CURRENT APPLICATION NUMBER: US/09/802,807
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/084,663
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (14)
; OTHER INFORMATION: n = A,T,C or G
US-09-802-807-7

Query Match      30.0%; Score 3; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
Db      10 RRR 8
      |||

RESULT 153
US-09-845-020A-8
; Sequence 8, Application US/09845020A
; Publication No. US20030022850A1
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michel W.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: Genomic Sequences for Protein Production
; TITLE OF INVENTION: and Delivery
; FILE REFERENCE: 50010/017003
; CURRENT APPLICATION NUMBER: US/09/845,020A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 09/305,384
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: US 60/084,649
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (14)
```

```
; OTHER INFORMATION: n=A,T,C or G
US-09-845-020A-8

Query Match      30.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
      |||
Db      1 YYY 3

RESULT 154
US-09-845-020A-8/c
; Sequence 8, Application US/09845020A
; Publication No. US20030022850A1
; GENERAL INFORMATION:
; APPLICANT: Ireco, Douglas A.
; APPLICANT: Heartlein, Michel W.
; APPLICANT: Seiden, Richard F
; TITLE OF INVENTION: Genomic Sequences for Protein Production
; TITLE OF INVENTION: and Delivery
; FILE REFERENCE: 50010/017003
; CURRENT APPLICATION NUMBER: US/09/845,020A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 09/305,384
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: US 60/084,649
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(14)
; OTHER INFORMATION: n=A,T,C or G
US-09-845-020A-8

Query Match      30.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
      |||
Db      10 RRR 8

RESULT 155
US-10-345-115-1
; Sequence 1, Application US/10345115
; Publication No. US20030224519A1
; GENERAL INFORMATION:
; APPLICANT: Harrington, John
; APPLICANT: Jackson, Paul David
; APPLICANT: Jiang, Li
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING
; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS
; FILE REFERENCE: ATX-004CP2
; CURRENT APPLICATION NUMBER: US/10/345,115
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 10/277612
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/336497
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 10/196721
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 11
; OTHER INFORMATION: n = A,T,C or G
US-10-345-115-1

Query Match      30.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
      |||
Db      10 RRR 8

RESULT 157
US-10-277-612-1
; Sequence 1, Application US/10277612
; Publication No. US20040018624A1
; GENERAL INFORMATION:
; APPLICANT: Harrington, John
; APPLICANT: Jackson, Paul David
; APPLICANT: Jiang, Li
```

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING  
;; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS  
;; FILE REFERENCE: ATX-004CP  
;; CURRENT APPLICATION NUMBER: US/10/277,612  
;; CURRENT FILING DATE: 2003-02-03  
;; PRIOR APPLICATION NUMBER: 60/336497  
;; PRIOR FILING DATE: 2001-10-22  
;; PRIOR APPLICATION NUMBER: 10/196721  
;; PRIOR FILING DATE: 2002-07-15  
;; NUMBER OF SEQ ID NOS: 1  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 14  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: 11  
;; OTHER INFORMATION: n = A,T,C or G  
;; NAME/KEY: misc\_feature  
;; LOCATION: 1-10;12  
;; OTHER INFORMATION: Y = C or T  
US-10-277-612-1

Query Match 30.0%; Score 3; DB 16; Length 14;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
|||  
Db 1 YYY 3

RESULT 158  
US-10-277-612-1/c  
;; Sequence 1, Application US/10277612  
;; Publication No. US20040018624A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Harrington, John  
;; APPLICANT: Jackson, Paul David  
;; APPLICANT: Jiang, Li  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING  
;; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS  
;; FILE REFERENCE: ATX-004CP  
;; CURRENT APPLICATION NUMBER: US/10/277,612  
;; CURRENT FILING DATE: 2003-02-03  
;; PRIOR APPLICATION NUMBER: 60/336497  
;; PRIOR FILING DATE: 2001-10-22  
;; PRIOR APPLICATION NUMBER: 10/196721  
;; PRIOR FILING DATE: 2002-07-15  
;; NUMBER OF SEQ ID NOS: 1  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 14  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: 11  
;; OTHER INFORMATION: n = A,T,C or G  
;; NAME/KEY: misc\_feature  
;; LOCATION: 1-10;12  
;; OTHER INFORMATION: Y = C or T  
US-10-277-612-1

Query Match 30.0%; Score 3; DB 16; Length 14;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
|||

Db 10 RRR 8

RESULT 159  
US-10-333-892-6  
;; Sequence 6, Application US/10333892  
;; Publication No. US20040209254A1  
;; GENERAL INFORMATION:  
;; APPLICANT: DZGenes LLC  
;; TITLE OF INVENTION: DIAGNOSTIC POLYMORPHISMS FOR THE TGF-BETA 1 PROMOTER  
;; FILE REFERENCE: DZG2185.2  
;; CURRENT APPLICATION NUMBER: US/10/333,892  
;; CURRENT FILING DATE: 2003-06-24  
;; PRIOR APPLICATION NUMBER: US 60/220,583  
;; PRIOR FILING DATE: 2000-07-25  
;; PRIOR APPLICATION NUMBER: PCT/US01/23368  
;; PRIOR FILING DATE: 2001-07-25  
;; NUMBER OF SEQ ID NOS: 6  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 6  
;; LENGTH: 14  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (11)..(11)  
;; OTHER INFORMATION: n=any nucleotide  
;; FEATURE:  
;; NAME/KEY: variation  
;; LOCATION: (6)..(6)  
;; OTHER INFORMATION: SNP replaces Y with a G at this position  
US-10-333-892-6

Query Match 30.0%; Score 3; DB 18; Length 14;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
|||  
Db 6 YYY 8

RESULT 160  
US-10-333-892-6/c  
;; Sequence 6, Application US/10333892  
;; Publication No. US20040209254A1  
;; GENERAL INFORMATION:  
;; APPLICANT: DZGenes LLC  
;; TITLE OF INVENTION: DIAGNOSTIC POLYMORPHISMS FOR THE TGF-BETA 1 PROMOTER  
;; FILE REFERENCE: DZG2185.2  
;; CURRENT APPLICATION NUMBER: US/10/333,892  
;; CURRENT FILING DATE: 2003-06-24  
;; PRIOR APPLICATION NUMBER: US 60/220,583  
;; PRIOR FILING DATE: 2000-07-25  
;; PRIOR APPLICATION NUMBER: PCT/US01/23368  
;; PRIOR FILING DATE: 2001-07-25  
;; NUMBER OF SEQ ID NOS: 6  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 6  
;; LENGTH: 14  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (11)..(11)  
;; OTHER INFORMATION: n=any nucleotide  
;; FEATURE:  
;; NAME/KEY: variation  
;; LOCATION: (6)..(6)  
;; OTHER INFORMATION: SNP replaces Y with a G at this position  
US-10-333-892-6

Query Match 30.0%; Score 3; DB 18; Length 14;





APPLICANT: Jackson, Paul David  
; APPLICANT: Jiang, Li  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING  
; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS  
; FILE REFERENCE: ATX-004CPCN4  
; CURRENT APPLICATION NUMBER: US/10/342,923  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: 10/277612  
; PRIOR FILING DATE: 2002-10-22  
; PRIOR APPLICATION NUMBER: 60/336497  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 10/196721  
; PRIOR FILING DATE: 2002-07-15  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 11  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1-10,12  
; OTHER INFORMATION: Y = C or T  
US-10-342-923-1

Query Match 30.0%; Score 3; DB 18; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
|||  
Db 10 RRR 8

## RESULT 165

US-10-342-948-1  
; Sequence 1, Application US/10342948  
; Publication No. US20040253591A1  
; GENERAL INFORMATION:  
; APPLICANT: Harrington, John  
; APPLICANT: Jackson, Paul David  
; APPLICANT: Jiang, Li  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING  
; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS  
; FILE REFERENCE: ATX-004CPCN3  
; CURRENT APPLICATION NUMBER: US/10/342,948  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: 10/277612  
; PRIOR FILING DATE: 2002-10-22  
; PRIOR APPLICATION NUMBER: 60/336497  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 10/196721  
; PRIOR FILING DATE: 2002-07-15  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 11  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1-10,12  
; OTHER INFORMATION: Y = C or T  
US-10-342-948-1

Query Match 30.0%; Score 3; DB 18; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10  
|||  
Db 1 YYY 3

## RESULT 166

US-10-342-948-1/c  
; Sequence 1, Application US/10342948  
; Publication No. US20040253591A1  
; GENERAL INFORMATION:  
; APPLICANT: Harrington, John  
; APPLICANT: Jackson, Paul David  
; APPLICANT: Jiang, Li  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING  
; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS  
; FILE REFERENCE: ATX-004CPCN3  
; CURRENT APPLICATION NUMBER: US/10/342,948  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: 10/277612  
; PRIOR FILING DATE: 2002-10-22  
; PRIOR APPLICATION NUMBER: 60/336497  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 10/196721  
; PRIOR FILING DATE: 2002-07-15  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 14  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 11  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1-10,12  
; OTHER INFORMATION: Y = C or T  
US-10-342-948-1

Query Match 30.0%; Score 3; DB 18; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3  
|||  
Db 10 RRR 8

## RESULT 167

US-10-418-182-183  
; Sequence 183, Application US/10418182  
; Publication No. US20030228302A1  
; GENERAL INFORMATION:  
; APPLICANT: Crea, Roberto  
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS  
; FILE REFERENCE: 1551.2001-001  
; CURRENT APPLICATION NUMBER: US/10/418,182  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/373,558  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 183  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide

## US-10-418-182-183

Query Match 30.0%; Score 3; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 RRC 4  
Db 1 RRC 3

## RESULT 168

US-10-418-182-183/c  
; Sequence 183, Application US/10418182  
; Publication No. US20030228302A1  
; GENERAL INFORMATION:  
; APPLICANT: Crea, Roberto  
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS  
; FILE REFERENCE: 1551.2001-001  
; CURRENT APPLICATION NUMBER: US/10/418,182  
; PRIOR FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/373,558  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 183  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide  
US-10-418-182-183

Query Match 30.0%; Score 3; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9  
Db 3 GY 1

## RESULT 169

US-10-418-182-219  
; Sequence 219, Application US/10418182  
; Publication No. US20030228302A1  
; GENERAL INFORMATION:  
; APPLICANT: Crea, Roberto  
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS  
; FILE REFERENCE: 1551.2001-001  
; CURRENT APPLICATION NUMBER: US/10/418,182  
; PRIOR FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/373,558  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 219  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide  
US-10-418-182-219

Query Match 30.0%; Score 3; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 6  
Db 3 CW 5

## RESULT 170

US-10-418-182-219/c  
; Sequence 219, Application US/10418182  
; Publication No. US20030228302A1  
; GENERAL INFORMATION:  
; APPLICANT: Crea, Roberto  
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS  
; FILE REFERENCE: 1551.2001-001  
; CURRENT APPLICATION NUMBER: US/10/418,182  
; PRIOR FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/373,558  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 219  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide  
US-10-418-182-219

Query Match 30.0%; Score 3; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7  
Db 5 WWG 3

## RESULT 171

US-10-418-182-313  
; Sequence 313, Application US/10418182  
; Publication No. US20030228302A1  
; GENERAL INFORMATION:  
; APPLICANT: Crea, Roberto  
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS  
; FILE REFERENCE: 1551.2001-001  
; CURRENT APPLICATION NUMBER: US/10/418,182  
; PRIOR FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/373,558  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 313  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide  
US-10-418-182-313

Query Match 30.0%; Score 3; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
Db 1 RRC 3

## RESULT 172

US-10-418-182-313/c  
; Sequence 313, Application US/10418182  
; Publication No. US20030228302A1  
; GENERAL INFORMATION:  
; APPLICANT: Crea, Roberto  
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS  
; FILE REFERENCE: 1551.2001-001  
; CURRENT APPLICATION NUMBER: US/10/418,182  
; PRIOR FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/373,558

; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 313  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide  
US-10-418-182-313

Query Match 30.0%; Score 3; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 9  
|||  
Db 3 GY 1

RESULT 173  
US-10-418-182-421  
; Sequence 421, Application US/10418182  
; Publication No. US20030228302A1  
; GENERAL INFORMATION:  
; APPLICANT: Crea, Roberto  
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS  
; FILE REFERENCE: 1551.2001-001  
; CURRENT APPLICATION NUMBER: US/10/418,182  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/373,558  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 421  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide  
US-10-418-182-421

Query Match 30.0%; Score 3; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 6  
|||  
Db 3 CW 5

RESULT 174  
US-10-418-182-421/c  
; Sequence 421, Application US/10418182  
; Publication No. US20030228302A1  
; GENERAL INFORMATION:  
; APPLICANT: Crea, Roberto  
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS  
; FILE REFERENCE: 1551.2001-001  
; CURRENT APPLICATION NUMBER: US/10/418,182  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/373,558  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 423  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 421  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide  
US-10-418-182-421

Query Match 30.0%; Score 3; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WW 7  
|||  
Db 5 WW 3

RESULT 175  
US-10-706-466-5  
; Sequence 5, Application US/10706466  
; Publication No. US20040082535A1  
; GENERAL INFORMATION:  
; APPLICANT: MAHURAN, Don J.  
; APPLICANT: CLARKE, Joe T.R.  
; APPLICANT: CALLAHAN, John W.  
; TITLE OF INVENTION: PRODUCTS AND METHODS FOR GAUCHER DISEASE THERAPY  
; FILE REFERENCE: 24,131 USA  
; CURRENT APPLICATION NUMBER: US/10/706,466  
; CURRENT FILING DATE: 2003-11-12  
; PRIOR APPLICATION NUMBER: 09/586,216  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/137,598  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 2,272,055  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc difference  
; LOCATION: y=1-10; n=11  
; OTHER INFORMATION: y=c or u; n=any nucleotide  
US-10-706-466-5

Query Match 30.0%; Score 3; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YY 10  
|||  
Db 1 YY 3

RESULT 176  
US-10-706-466-5/c  
; Sequence 5, Application US/10706466  
; Publication No. US20040082535A1  
; GENERAL INFORMATION:  
; APPLICANT: MAHURAN, Don J.  
; APPLICANT: CLARKE, Joe T.R.  
; APPLICANT: CALLAHAN, John W.  
; TITLE OF INVENTION: PRODUCTS AND METHODS FOR GAUCHER DISEASE THERAPY  
; FILE REFERENCE: 24,131 USA  
; CURRENT APPLICATION NUMBER: US/10/706,466  
; CURRENT FILING DATE: 2003-11-12  
; PRIOR APPLICATION NUMBER: 09/586,216  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/137,598  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 2,272,055  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: misc difference  
; LOCATION: Y=1-10; n=11  
; OTHER INFORMATION: Y=c or u; n=any nucleotide  
US-10-706-466-5

Query Match 30.0%; Score 3; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
Db 10 RRR 8

## RESULT 177

US-09-754-014-11/c  
; Sequence 11, Application US/09754014  
; Patent No. US20020119940A1  
; GENERAL INFORMATION:  
; APPLICANT: Jeff No. US20020119940A1dstrom  
; Bruce Freimark  
; Deepa Deshpande  
; TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYSTEMS  
; AND USES

NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/754,014  
FILING DATE: 03-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/948,958  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Berkman, Charles S.  
REGISTRATION NUMBER: 38,077  
REFERENCE/DOCKET NUMBER: 226/284  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
OTHER INFORMATION: The letter "Y" stands for C or T.  
The letter "N" stands for any base.

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

## US-09-754-014-11

Query Match 30.0%; Score 3; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10  
Db 1 YYY 3

## RESULT 178

US-09-754-014-11/c  
; Sequence 11, Application US/09754014  
; Patent No. US20020119940A1  
; GENERAL INFORMATION:  
; APPLICANT: Jeff No. US20020119940A1dstrom  
; Bruce Freimark  
; Deepa Deshpande

TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYSTEMS  
AND USES

NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/754,014  
FILING DATE: 03-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/948,958  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Berkman, Charles S.  
REGISTRATION NUMBER: 38,077  
REFERENCE/DOCKET NUMBER: 226/284  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
OTHER INFORMATION: The letter "Y" stands for C or T.  
The letter "N" stands for any base.

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

## US-09-754-014-11

Query Match 30.0%; Score 3; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3  
Db 11 RRR 9

## RESULT 179

US-09-836-866-7  
; Sequence 7, Application US/09836866  
; Patent No. US20020123473A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20020123473A1dstrom, Jeff  
; Freimark, Bruce  
; Deshpande, Deepa

TITLE OF INVENTION: IL-12 GENE EXPRESSION AND  
DELIVERY SYSTEMS AND USES



US-09-892-867-5/c  
; Sequence 5, Application US/09892867  
; Patent No. US20020037568A1  
; GENERAL INFORMATION:

; APPLICANT: MOLENAAR, DOUWE  
; APPLICANT: VAN DER REST, MICHEL E  
; APPLICANT: DRYSCH, ANDRE  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE WHICH CODE FOR THE mdhA GENE  
; FILE REFERENCE: 203576USOX  
; CURRENT APPLICATION NUMBER: US/09/892,867  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: DE 100322350.2  
; PRIOR FILING DATE: 2000-07-04  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic DNA  
US-09-892-867-5

Query Match 30.0%; Score 3; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9  
|||  
Db 16 GY 14

## RESULT 183

US-09-973-451-15  
; Sequence 15, Application US/09973451  
; Patent No. US20020132328A1  
; GENERAL INFORMATION:  
; APPLICANT: JACOBSON, Myron K.  
; APPLICANT: JACOBSON, Elaine L.  
; APPLICANT: AM, Jean-Christophe  
; APPLICANT: LIN, Winston  
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE  
; TITLE OF INVENTION: (PARG) ENZYMES,  
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV  
; TITLE OF INVENTION: THEREWITH  
; FILE REFERENCE: NIAD 201  
; CURRENT APPLICATION NUMBER: US/09/973,451  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: US/09/302,812  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/083,768  
; PRIOR FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 38  
; SEQ ID NO 15  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; FEATURE:  
US-09-973-451-15

Query Match 30.0%; Score 3; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9  
|||  
Db 14 GY 16

## RESULT 184

US-09-973-451-15/c  
; Sequence 15, Application US/09973451  
; Patent No. US20020132328A1

; GENERAL INFORMATION:  
; APPLICANT: JACOBSON, Myron K.  
; APPLICANT: JACOBSON, Elaine L.  
; APPLICANT: AM, Jean-Christophe  
; APPLICANT: LIN, Winston  
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE  
; TITLE OF INVENTION: (PARG) ENZYMES,  
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV  
; TITLE OF INVENTION: THEREWITH  
; FILE REFERENCE: NIAD 201  
; CURRENT APPLICATION NUMBER: US/09/973,451  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: US/09/302,812  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/083,768  
; PRIOR FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 38  
; SEQ ID NO 15  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; FEATURE:  
US-09-973-451-15

Query Match 30.0%; Score 3; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4  
|||  
Db 16 RRC 14

## RESULT 185

US-09-836-705-4  
; Sequence 4, Application US/09836705  
; Publication No. US20030078395A1  
; GENERAL INFORMATION:  
; APPLICANT: Abe, Yuki  
; APPLICANT: Ono, Chiho  
; APPLICANT: Yoshioka, Hiroji  
; TITLE OF INVENTION: Genes from a Gene Cluster  
; FILE REFERENCE: 01149/HG  
; CURRENT APPLICATION NUMBER: US/09/836,705  
; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: JP 2000-116591  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: JP 2000-117458  
; PRIOR FILING DATE: 2000-04-19  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Description of Artificial Sequence: A mixed primer  
; OTHER INFORMATION: which has a DNA sequence deduced from the amino  
; OTHER INFORMATION: acid sequence of PKS of Aspergillus flavus.  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: i  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (6)..(6)  
; OTHER INFORMATION: i  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: i  
; FEATURE:

```
; NAME/KEY: modified base
; LOCATION: (15)..(15)
; OTHER INFORMATION: 1
US-09-836-705-4

Query Match      30.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RCW 5
      |||
Db      9 RCW 11

RESULT 186
US-09-836-705-4/c
; Sequence 4, Application US/09836705
; Publication No. US20030078395A1
; GENERAL INFORMATION:
; APPLICANT: Abe, Yuki
; APPLICANT: Ono, Chiho
; APPLICANT: Yoshikawa, Hiroji
; TITLE OF INVENTION: Genes from a Gene Cluster
; FILE REFERENCE: 01149/HG
; CURRENT APPLICATION NUMBER: US/09/836,705
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: JP 2000-116591
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: JP 2000-117458
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: A mixed primer
; OTHER INFORMATION: which has a DNA sequence deduced from the amino
; OTHER INFORMATION: acid sequence of PKS of Aspergillus flavus.
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (3)..(3)
; OTHER INFORMATION: 1
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(6)
; OTHER INFORMATION: 1
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: 1
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (15)..(15)
; OTHER INFORMATION: 1
US-09-836-705-4

Query Match      30.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WGY 8
      |||
Db      11 WGY 9

RESULT 187
US-09-903-770-5
; Sequence 5, Application US/09903770
; Publication No. US20030170780A1
; GENERAL INFORMATION:
; APPLICANT: MOLENAAR, DOUWE
; APPLICANT: VAN DER REST, MICHEL E
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE WHICH CODE FOR THE mdhA GENE
; FILE REFERENCE: 203976US0X
; CURRENT APPLICATION NUMBER: US/09/903,770
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: DE 10032350.2
; PRIOR FILING DATE: 2000-07-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-09-903-770-5

Query Match      30.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GYV 9
      |||
Db      16 GYV 14

RESULT 189
US-09-876-813-10
; Sequence 10, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
```

```

; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(17)
; OTHER INFORMATION: n = A,T,C or G
US-09-876-813-10

```

```

Query Match      30.0%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 GYY 9
      |||
Db     14 GYY 16

```

## RESULT 190

```

US-09-876-813-10/c
; Sequence 10, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(17)
; OTHER INFORMATION: n = A,T,C or G
US-09-876-813-10

```

```

Query Match      30.0%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 RRC 4
      |||
Db     16 RRC 14

```

## RESULT 191

```

US-10-043-142-1
; Sequence 1, Application US/10043142
; Publication No. US20020150969A1
; GENERAL INFORMATION:
; APPLICANT: DERKX, PATRICK M.F.
; APPLICANT: MADRID, SUSAN M.
; TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
; FILE REFERENCE: 078883/0128
; CURRENT APPLICATION NUMBER: US/10/043,142
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 09/806,399
; PRIOR FILING DATE: 2002-03-30
; PRIOR APPLICATION NUMBER: PCT/IB99/01669
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: GB 9821198.0
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-043-142-1

```

```

Query Match      30.0%; Score 3; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 GYY 9
      |||
Db     2 GYY 4

```

## RESULT 192

```

US-10-043-142-1/c
; Sequence 1, Application US/10043142
; Publication No. US20020150969A1
; GENERAL INFORMATION:
; APPLICANT: DERKX, PATRICK M.F.
; APPLICANT: MADRID, SUSAN M.
; TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
; FILE REFERENCE: 078883/0128
; CURRENT APPLICATION NUMBER: US/10/043,142
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 09/806,399
; PRIOR FILING DATE: 2002-03-30
; PRIOR APPLICATION NUMBER: PCT/IB99/01669
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: GB 9821198.0
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-043-142-1

```

```

Query Match      30.0%; Score 3; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 RRC 4
      |||
Db     4 RRC 2

```



RESULT 193  
US-10-139-583-10  
; Sequence 10, Application US/10139583  
; Publication No. US20020177193A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/10/139,583  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 09/457,066  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(17)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-139-583-10

Query Match 30.0%; Score 3; DB 13; Length 17;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 GY 9  
|||  
Db 14 GY 16

RESULT 194  
US-10-139-583-10/c  
; Sequence 10, Application US/10139583  
; Publication No. US20020177193A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/10/139,583  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 09/457,066  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(17)  
; OTHER INFORMATION: n = A,T,C or G

US-10-139-583-10  
  
Query Match 30.0%; Score 3; DB 13; Length 17;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 RRC 4  
|||  
Db 16 RRC 14  
  
RESULT 195  
US-10-338-237-16  
; Sequence 16, Application US/10338237  
; Publication No. US20030148357A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lok, Si  
; TITLE OF INVENTION: NOVEL CYSTINE KNOT PROTEIN AND MATERIALS  
; FILE REFERENCE: 97-65  
; CURRENT APPLICATION NUMBER: US/10/338,237  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: US/09/250,124A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,682  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/102,709  
; PRIOR FILING DATE: 1998-10-01  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide primer  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (1)..(17)  
; OTHER INFORMATION: n is any nucleotide  
US-10-338-237-16

Query Match 30.0%; Score 3; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 RCW 5  
|||  
Db 5 RCW 7  
  
RESULT 196  
US-10-338-237-16/c  
; Sequence 16, Application US/10338237  
; Publication No. US20030148357A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lok, Si  
; TITLE OF INVENTION: NOVEL CYSTINE KNOT PROTEIN AND MATERIALS  
; FILE REFERENCE: 97-65  
; CURRENT APPLICATION NUMBER: US/10/338,237  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: US/09/250,124A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,682  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/102,709  
; PRIOR FILING DATE: 1998-10-01  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16

```
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
;
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(17)
; OTHER INFORMATION: n is any nucleotide
US-10-338-237-16

Query Match          30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WGY 8
      |||
Db      7 WGY 5

RESULT 197
US-10-302-554-29
; Sequence 29, Application US/10302554
; Publication No. US20030148467A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4
; FILE REFERENCE: 98-59
; CURRENT APPLICATION NUMBER: US/10/302,554
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US/09/428,118
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 60/105,824
; PRIOR FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(17)
; OTHER INFORMATION: n is any nucleotide
; OTHER INFORMATION: oligonucleotide primer
US-10-302-554-29

Query Match          30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GY 9
      |||
Db      8 GY 10

RESULT 198
US-10-302-554-29/c
; Sequence 29, Application US/10302554
; Publication No. US20030148467A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4
; FILE REFERENCE: 98-59
; CURRENT APPLICATION NUMBER: US/10/302,554
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US/09/428,118
; PRIOR FILING DATE: 1999-10-27

; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(17)
; OTHER INFORMATION: n is any nucleotide
; OTHER INFORMATION: oligonucleotide primer
US-10-302-554-29

Query Match          30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GY 9
      |||
Db      8 GY 10

RESULT 199
US-10-404-300A-28
; Sequence 28, Application US/10404300A
; Publication No. US20030215856A1
; GENERAL INFORMATION:
; APPLICANT: Church, George
; APPLICANT: Bullyk, Martha
; TITLE OF INVENTION: SURFACE-BOUND, DOUBLE-STRANDED DNA PROTEIN ARRAYS
; FILE REFERENCE: 10498-00050
; CURRENT APPLICATION NUMBER: US/10/404,300A
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 09/132,368
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/061,604
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 28
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: n is a, c, g or t
US-10-404-300A-28

Query Match          30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CWW 6
      |||
Db      6 CWW 8

RESULT 200
US-10-404-300A-28/c
; Sequence 28, Application US/10404300A
; Publication No. US20030215856A1
; GENERAL INFORMATION:
; APPLICANT: Church, George
; APPLICANT: Bullyk, Martha
; TITLE OF INVENTION: SURFACE-BOUND, DOUBLE-STRANDED DNA PROTEIN ARRAYS
; FILE REFERENCE: 10498-00050
; CURRENT APPLICATION NUMBER: US/10/404,300A
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 09/132,368
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; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/061,604
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: n is a, c, g or t
US-10-404-300A-28
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Query Match      30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      4 CWW 6
      |||
Db      12 CWW 10
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Search completed: January 14, 2005, 19:05:52
Job time : 403 secs
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